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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: (OTHER THAN US): FLORIGENE LIMITED

(US ONLY): Filippa BRUGLIERA, Timothy Albert HOLTON, Michael Zeron MICHAEL

(ii) TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES AND USES THEREFOR

(iii) NUMBER OF SEQUENCES: 40

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DAVIES COLLISON CAVE

(B) STREET: 1 LITTLE COLLINS STREET

(C) CITY: MELBOURNE

(D) STATE: VICTORIA

(E) COUNTRY: AUSTRALIA

(F) ZIP: 3000

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

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(B) FILING DATE: 28-FEB-1997

(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PN8386

(B) FILING DATE: 28-FEB-1997

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: HUGHES, DR E JOHN L

(C) REFERENCE/DOCKET NUMBER: EJH/AF

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: +61 3 9254 2777

(B) TELEFAX: +61 3 9254 2770

(C) TELEX: AA 31787

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1789 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 50..1586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCAGGAATTG GTGAAACCCCA TAGAAGTAAA ATACTCCTAT CTTTATTC ATG GAA	55		
	Met Glu		
	1		
ATC TTA AGC CTA ATT CTG TAC ACC GTC ATT TTC TCA TTT CTT CTA CAA	103		
Ile Leu Ser Leu Ile Leu Tyr Thr Val Ile Phe Ser Phe Leu Leu Gln			
5	10	15	
TTC ATT CTT AGA TCA TTT TTC CGT AAA CGT TAC CCT TTA CCA TTA CCA	151		
Phe Ile Leu Arg Ser Phe Phe Arg Lys Arg Tyr Pro Leu Pro Leu Pro			
20	25	30	
CCA GGT CCA AAA CCA TGG CCA ATT ATA GGA AAC CTA GTC CAT CTT GGA	199		
Pro Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His Leu Gly			
35	40	45	50
CCC AAA CCA CAT CAA TCA ACT GCA GCC ATG GCT CAA ACT TAT GGA CCA	247		
Pro Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr Gly Pro			
55	60	65	

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CTC ATG TAT CTT AAG ATG GGG TTC GTA GAC GTG GTG GTT GCA GCC TCG			295
Leu Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Val Ala Ala Ser			
70	75	80	
GCA TCG GTT GCA GCT CAG TTC TTG AAA ACT CAT GAT GCT AAT TTC TCG			343
Ala Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn Phe Ser			
85	90	95	
AGC CGT CCA CCA AAT TCT GGT GCA GAA CAT ATG GCT TAT AAT TAT CAG			391
Ser Arg Pro Pro Asn Ser Gly Ala Glu His Met Ala Tyr Asn Tyr Gln			
100	105	110	
GAT CTT GTT TTT GCA CCT TAT GGA CCT AGA TGG CGT ATG CTT AGG AAA			439
Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu Arg Lys			
115	120	125	130
ATT TGC TCA GTT CAC CTT TTC TCT ACC AAG GCT TTA GAT GAC TTC CGC			487
Ile Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp Phe Arg			
135	140	145	
CAT GTC CGC CAG GAT GAA GTG AAA ACA CTG ACG CGC GCA CTA GCA AGT			535
His Val Arg Gln Asp Glu Val Lys Thr Leu Thr Arg Ala Leu Ala Ser			
150	155	160	
GCA GGC CAA AAG CCA GTC AAA TTA GGT CAG TTA TTG AAC GTG TGC ACG			583
Ala Gly Gln Lys Pro Val Lys Leu Gly Gln Leu Leu Asn Val Cys Thr			
165	170	175	
ACG AAC GCA CTC GCG CGA GTA ATG CTA GGT AAG CGA GTA TTT GCC GAC			631
Thr Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe Ala Asp			
180	185	190	
GGA AGT GGC GAT GTT GAT CCA CAA GCG GCG GAG TTC AAG TCA ATG GTG			679
Gly Ser Gly Asp Val Asp Pro Gln Ala Ala Glu Phe Lys Ser Met Val			
195	200	205	210
GTG GAA ATG ATG GTA GTC GCC GGT GTT TTT AAC ATT GGT GAT TTT ATT			727

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Val Glu Met Met Val Val Ala Gly Val Phe Asn Ile Gly Asp Phe Ile			
215	220	225	
CCG CAA CTT AAT TGG TTA GAT ATT CAA GGT GTA GCC GCT AAA ATG AAG 775			
Pro Gln Leu Asn Trp Leu Asp Ile Gln Gly Val Ala Ala Lys Met Lys			
230	235	240	
AAG CTC CAC GCG CGT TTC GAC GCG TTC TTG ACT GAT ATA CTT GAA GAG 823			
Lys Leu His Ala Arg Phe Asp Ala Phe Leu Thr Asp Ile Leu Glu Glu			
245	250	255	
CAT AAG GGT AAA ATT TTT GGA GAA ATG AAA GAT TTG TTG AGT ACT TTG 871			
His Lys Gly Lys Ile Phe Gly Glu Met Lys Asp Leu Leu Ser Thr Leu			
260	265	270	
ATC TCT CTT AAA AAT GAT GAT GCG GAT AAT GAT GGA GGG AAA CTC ACT 919			
Ile Ser Leu Lys Asn Asp Asp Ala Asp Asn Asp Gly Gly Lys Leu Thr			
275	280	285	290
GAT ACA GAA ATT AAA GCA TTA CTT TTG AAC TTG TTT GTA GCT GGA ACA 967			
Asp Thr Glu Ile Lys Ala Leu Leu Asn Leu Phe Val Ala Gly Thr			
295	300	305	
GAC ACA TCT TCT AGT ACA GTT GAA TGG GCC ATT GCT GAG CTT ATT CGT 1015			
Asp Thr Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg			
310	315	320	
AAT CCA AAA ATA CTA GCC CAA GCC CAG CAA GAG ATC GAC AAA GTC GTT 1063			
Asn Pro Lys Ile Leu Ala Gln Ala Gln Gln Glu Ile Asp Lys Val Val			
325	330	335	
GGA AGG GAC CGG CTA GTT GGC GAA TTG GAC CTA GCC CAA TTG ACA TAC 1111			
Gly Arg Asp Arg Leu Val Gly Glu Leu Asp Leu Ala Gln Leu Thr Tyr			
340	345	350	
TTG GAA GCT ATA GTC AAG GAA ACC TTT CGG CTT CAT CCA TCA ACC CCT 1159			
Leu Glu Ala Ile Val Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro			

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355	360	365	370
CTT TCA CTT CCT AGA ATT GCA TCT GAG AGT TGT GAG ATC AAT GGC TAT			
Leu Ser Leu Pro Arg Ile Ala Ser Glu Ser Cys Glu Ile Asn Gly Tyr			
375	380	385	
TTC ATT CCA AAA GGC TCA ACG CTT CTC CTT AAT GTT TGG GCC ATT GCT			
Phe Ile Pro Lys Gly Ser Thr Leu Leu Leu Asn Val Trp Ala Ile Ala			
390	395	400	
CGT GAT CCA AAT GCA TGG GCT GAT CCA TTG GAG TTT AGG CCT GAA AGG			
Arg Asp Pro Asn Ala Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg			
405	410	415	
TTT TTG CCA GGA GGT GAG AAG CCC AAA GTT GAT GTC CGT GGG AAT GAC			
Phe Leu Pro Gly Gly Glu Lys Pro Lys Val Asp Val Arg Gly Asn Asp			
420	425	430	
TTT GAA GTC ATA CCA TTT GGA GCT GGA CGT AGG ATT TGT GCT GGA ATG			
Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met			
435	440	445	450
AAT TTG GGT ATA CGT ATG GTC CAG TTG ATG ATT GCA ACT TTA ATA CAT			
Asn Leu Gly Ile Arg Met Val Gln Leu Met Ile Ala Thr Leu Ile His			
455	460	465	
GCA TTT AAC TGG GAT TTG GTC AGT GGA CAA TTG CCG GAG ATG TTG AAT			
Ala Phe Asn Trp Asp Leu Val Ser Gly Gln Leu Pro Glu Met Leu Asn			
470	475	480	
ATG GAA GAA GCA TAT GGG CTG ACC TTA CAA CGG GCT GAT CCA TTG GTT			
Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro Leu Val			
485	490	495	
GTG CAC CCA AGG CCT CGC TTA GAA GCC CAA GCG TAC ATT GGG T			
Val His Pro Arg Pro Arg Leu Glu Ala Gln Ala Tyr Ile Gly			
500	505	510	

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GAGCAGCAAC AGCCCATGGA GATAACATGA GTGTTAAATG TATGAGTCTC CATACTTG	1646
TTAGTTGTT TATGCTTGG ATTTAGTAGT TTTTATATTG ATAGATCAAT GTTGCATTG	1706
TCAGTAAGAA TATCCGTTGC TTGTTTCATT AACTCCAGGT GGACAATAAA AGAAGTAATT	1766
TGTATGAAAA AAAAAAAA AAA	1789

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Ile Leu Ser Leu Ile Leu Tyr Thr Val Ile Phe Ser Phe Leu			
1	5	10	15

Leu Gln Phe Ile Leu Arg Ser Phe Phe Arg Lys Arg Tyr Pro Leu Pro		
20	25	30

Leu Pro Pro Gly Pro Lys Pro Trp Pro Ile Ile .Gly Asn Leu Val His		
35	40	45

Leu Gly Pro Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr		
50	55	60

Gly Pro Leu Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Val Ala			
65	70	75	80

Ala Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn		
85	90	95

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Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Glu His Met Ala Tyr Asn
100 105 110

Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu
115 120 125

Arg Lys Ile Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp
130 135 140

Phe Arg His Val Arg Gln Asp Glu Val Lys Thr Leu Thr Arg Ala Leu
145 150 155 160

Ala Ser Ala Gly Gln Lys Pro Val Lys Leu Gly Gln Leu Leu Asn Val
165 170 175

Cys Thr Thr Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe
180 185 190

Ala Asp Gly Ser Gly Asp Val Asp Pro Gln Ala Ala Glu Phe Lys Ser
195 200 205

Met Val Val Glu Met Met Val Val Ala Gly Val Phe Asn Ile Gly Asp
210 215 220

Phe Ile Pro Gln Leu Asn Trp Leu Asp Ile Gln Gly Val Ala Ala Lys
225 230 235 240

Met Lys Lys Leu His Ala Arg Phe Asp Ala Phe Leu Thr Asp Ile Leu
245 250 255

Glu Glu His Lys Gly Lys Ile Phe Gly Glu Met Lys Asp Leu Leu Ser
260 265 270

Thr Leu Ile Ser Leu Lys Asn Asp Asp Ala Asp Asn Asp Gly Gly Lys
275 280 285

Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Val Ala

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290

295

300

Gly Thr Asp Thr Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu

305

310

315

320

Ile Arg Asn Pro Lys Ile Leu Ala Gln Ala Gln Gln Glu Ile Asp Lys

325

330

335

Val Val Gly Arg Asp Arg Leu Val Gly Glu Leu Asp Leu Ala Gln Leu

340

345

350

Thr Tyr Leu Glu Ala Ile Val Lys Glu Thr Phe Arg Leu His Pro Ser

355

360

365

Thr Pro Leu Ser Leu Pro Arg Ile Ala Ser Glu Ser Cys Glu Ile Asn

370

375

380

Gly Tyr Phe Ile Pro Lys Gly Ser Thr Leu Leu Leu Asn Val Trp Ala

385

390

395

400

Ile Ala Arg Asp Pro Asn Ala Trp Ala Asp Pro Leu Glu Phe Arg Pro

405

410

415

Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Lys Val Asp Val Arg Gly

420

425

430

Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala

435

440

445

Gly Met Asn Leu Gly Ile Arg Met Val Gln Leu Met Ile Ala Thr Leu

450

455

460

Ile His Ala Phe Asn Trp Asp Leu Val Ser Gly Gln Leu Pro Glu Met

465

470

475

480

Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro

485

490

495

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Leu Val Val His Pro Arg Pro Arg Leu Glu Ala Gln Ala Tyr Ile Gly
 500 505 510

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 172..1660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGTTCGGCA CGAGCGTCAC ATTACACACCG TCACATTACT ATTCAAACCA CTCATTTCT 60

ACCTCTCTTT TCTACCCACC AAAACAAAAC AAAACAAAAAA AAAACACATA AAAAAACTCA 120

AAAAAAAATT ATAATGTCAC CCTTAGAGGT AACTTCTAC ACCATAGTCC T ATG CAC 177

Met His

1

AAT CTC TAC TAC CTC ATC ACC ACC GTC TTC CGC GGC CAC CAA AAA CCG 225

Asn Leu Tyr Tyr Leu Ile Thr Thr Val Phe Arg Gly His Gln Lys Pro

5 10 15

CTT CCT CCA GGG CCA CGA CCA TGG CCC ATC GTG GGA AAC CTC CCA CAT 273

Leu Pro Pro Gly Pro Arg Pro Trp Pro Ile Val Gly Asn Leu Pro His

20 25 30

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ATG GGC CAG GCA CCG CAC CAG GGC TTA GCA GCC CTG GCG CAA AAG TAT			321
Met Gly Gln Ala Pro His Gln Gly Leu Ala Ala Leu Ala Gln Lys Tyr			
35	40	45	50
GGC CCT CTA TTG TAT ATG AGA CTG GGG TAC GTG GAC GTT GTG GCC			369
Gly Pro Leu Leu Tyr Met Arg Leu Gly Tyr Val Asp Val Val Val Ala			
55	60	65	
GCC TCA GCG TCT GTA GCG ACC CAG TTT CTT AAG ACA CAT GAC CTA AAT			417
Ala Ser Ala Ser Val Ala Thr Gln Phe Leu Lys Thr His Asp Leu Asn			
70	75	80	
TTT TCG AGT AGG CCA CCG AAT TCG GGG GCT AAA CAC ATT GCT TAT AAC			465
Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His Ile Ala Tyr Asn			
85	90	95	
TAT CAA GAC CTT GTT TTT GCA CCT TAT GGA CCT AAA TGG CGC ATG CTT			513
Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Lys Trp Arg Met Leu			
100	105	110	
AGG AAA ATT TGT TCC TTA CAC ATG TTT TCT TCT AAG GCT TTG GAC GAT			561
Arg Lys Ile Cys Ser Leu His Met Phe Ser Ser Lys Ala Leu Asp Asp			
115	120	125	130
TTT AGA CTT GTC CGT CAG GAA GAA GTA TCT ATA CTG GTA AAT GCG ATA			609
Phe Arg Leu Val Arg Gln Glu Glu Val Ser Ile Leu Val Asn Ala Ile			
135	140	145	
GCA AAA GCA GGA ACA AAG CCA GTA CAA CTA GGA CAA CTA CTC AAC GTG			657
Ala Lys Ala Gly Thr Lys Pro Val Gln Leu Gly Gln Leu Leu Asn Val			
150	155	160	
TGC ACC ACA AAT GCC TTA TCG AGG GTG ATG CTA GGG AAG CGA GTT CTC			705
Cys Thr Thr Asn Ala Leu Ser Arg Val Met Leu Gly Lys Arg Val Leu			
165	170	175	
GGT GAT GGC ACA GGG AAA AGC GAC CCA AAA GCC GAG GAA TTT AAG GAC			753

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Gly Asp Gly Thr Gly Lys Ser Asp Pro Lys Ala Glu Glu Phe Lys Asp

180 185 190

ATG GTG CTG GAG TTA ATG GTT CTC ACC GGA GTT TTT AAC ATT GGC GAT
Met Val Leu Glu Leu Met Val Leu Thr Gly Val Phe Asn Ile Gly Asp

195 200 205 210

TTT GTA CCG GCA TTG GAA TGT CTA GAC TTA CAA GGT GTT GCA TCT AAA
Phe Val Pro Ala Leu Glu Cys Leu Asp Leu Gln Gly Val Ala Ser Lys

215 220 225

ATG AAG AAA TTA CAT AAA AGA CTT GAT AAT TTT ATG AGT AAC ATT TTG
Met Lys Lys Leu His Lys Arg Leu Asp Asn Phe Met Ser Asn Ile Leu

230 235 240

GAG GAA CAC AAG AGT GTT GCA CAT CAA CAA AAT GGT GGA GAT TTG CTA
Glu Glu His Lys Ser Val Ala His Gln Gln Asn Gly Gly Asp Leu Leu

245 250 255

AGC ATT TTG ATA TCT TTG AAG GAT AAT TGT GAT GGT GAA GGT GGC AAG
Ser Ile Leu Ile Ser Leu Lys Asp Asn Cys Asp Gly Glu Gly Lys

260 265 270

TTT AGT GCC ACA GAA ATT AAG GCC TTG CTA TTG GAT TTA TTT ACA GCT
Phe Ser Ala Thr Glu Ile Lys Ala Leu Leu Leu Asp Leu Phe Thr Ala

275 280 285 290

GGA ACA GAC ACA TCA TCT AGT ACA ACT GAA TGG GCC ATA GCC GAA CTA
Gly Thr Asp Thr Ser Ser Ser Thr Thr Glu Trp Ala Ile Ala Glu Leu

295 300 305

ATT CGC CAT CCA AAA ATC TTA GCC CAA GTT CAA CAA GAA ATG GAC TCA
Ile Arg His Pro Lys Ile Leu Ala Gln Val Gln Gln Glu Met Asp Ser

310 315 320

GTC GTG GGC CGA GAC CGA CTC ATA GCC GAA GCT GAC ATA CCG AAC CTA
Val Val Gly Arg Asp Arg Leu Ile Ala Glu Ala Asp Ile Pro Asn Leu

801

849

897

945

993

1041

1089

1137

1185

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325	330	335	
ACC TAC TTC CAA GCC GTA ATC AAA GAG GTT TTC CGA CTT CAC CCG TCC Thr Tyr Phe Gln Ala Val Ile Lys Glu Val Phe Arg Leu His Pro Ser			1233
340	345	350	
ACC CCG CTT TCC CTA CCA CGG GTC GCA AAC GAA TCG TGC GAA ATA AAC Thr Pro Leu Ser Leu Pro Arg Val Ala Asn Glu Ser Cys Glu Ile Asn			1281
355	360	365	370
GGG TAC CAC ATT CCC AAA AAC ACC ACT TTA TTG GTA AAT GTG TGG GCC Gly Tyr His Ile Pro Lys Asn Thr Thr Leu Leu Val Asn Val Trp Ala			1329
375	380	385	
ATC GCA CGC GAC CCT GAG GTT TGG GCC GAC CCG TTA GAG TTT AAA CCC Ile Ala Arg Asp Pro Glu Val Trp Ala Asp Pro Leu Glu Phe Lys Pro			1377
390	395	400	
GAA AGA TTT TTG CCG GGC GGC GAA AAG CCC AAT GTG GAT GTG AAA GGA Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn Val Asp Val Lys Gly			1425
405	410	415	
AAC GAT TTT GAG CTG ATT CCG TTC GGG GCG GGC CGA CGG ATT TGT GCT Asn Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala			1473
420	425	430	
GGG CTG AGT TTG GGC CTG CGT ATG GTC CAG TTG ATG ACA GCC ACT TTG Gly Leu Ser Leu Gly Leu Arg Met Val Gln Leu Met Thr Ala Thr Leu			1521
435	440	445	450
GCC CAT ACT TAT GAT TGG GCC TTA GCT GAT GGG CTT ATG CCC GAA AAG Ala His Thr Tyr Asp Trp Ala Leu Ala Asp Gly Leu Met Pro Glu Lys			1569
455	460	465	
CTT AAC ATG GAT GAG GCT TAT GGG CTT ACC TTA CAG CGT AAG GTG CCA Leu Asn Met Asp Glu Ala Tyr Gly Leu Thr Leu Gln Arg Lys Val Pro			1617
470	475	480	

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CTT AAT GGT CCA CCC GAC CCC GTC GGC TTC TCG GCC CGT GTT T 1660
Leu Asn Gly Pro Pro Asp Pro Val Gly Phe Ser Ala Arg Val
485 490 495

AATAATTCCG GGGTTTTAA AAGCGGGTTA CTTTGTTTA TGTATTATTC CGTACTAGTT 1720

TGAAAATAAT GGTATTAGAG AAATG 1745

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met His Asn Leu Tyr Tyr Leu Ile Thr Thr Val Phe Arg Gly His Gln
1 5 10 15

Lys Pro Leu Pro Pro Gly Pro Arg Pro Trp Pro Ile Val Gly Asn Leu
20 25 30

Pro His Met Gly Gln Ala Pro His Gln Gly Leu Ala Ala Leu Ala Gln
35 40 45

Lys Tyr Gly Pro Leu Leu Tyr Met Arg Leu Gly Tyr Val Asp Val Val
50 55 60

Val Ala Ala Ser Ala Ser Val Ala Thr Gln Phe Leu Lys Thr His Asp
65 70 75 80

Leu Asn Phe S r Ser Arg Pro Pro Asn Ser Gly Ala Lys His Ile Ala
85 90 95

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Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Lys Trp Arg
100 105 110

Met Leu Arg Lys Ile Cys Ser Leu His Met Phe Ser Ser Lys Ala Leu
115 120 125

Asp Asp Phe Arg Leu Val Arg Gln Glu Glu Val Ser Ile Leu Val Asn
130 135 140

Ala Ile Ala Lys Ala Gly Thr Lys Pro Val Gln Leu Gly Gln Leu Leu
145 150 155 160

Asn Val Cys Thr Thr Asn Ala Leu Ser Arg Val Met Leu Gly Lys Arg
165 170 175

Val Leu Gly Asp Gly Thr Gly Lys Ser Asp Pro Lys Ala Glu Glu Phe
180 185 190

Lys Asp Met Val Leu Glu Leu Met Val Leu Thr Gly Val Phe Asn Ile
195 200 205

Gly Asp Phe Val Pro Ala Leu Glu Cys Leu Asp Leu Gln Gly Val Ala
210 215 220

Ser Lys Met Lys Lys Leu His Lys Arg Leu Asp Asn Phe Met Ser Asn
225 230 235 240

Ile Leu Glu Glu His Lys Ser Val Ala His Gln Gln Asn Gly Gly Asp
245 250 255

Leu Leu Ser Ile Leu Ile Ser Leu Lys Asp Asn Cys Asp Gly Glu Gly
260 265 270

Gly Lys Phe Ser Ala Thr Glu Ile Lys Ala Leu Leu Leu Asp Leu Phe
275 280 285

Thr Ala Gly Thr Asp Thr Ser Ser Ser Thr Thr Glu Trp Ala Ile Ala

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290	295	300	
Glu Leu Ile Arg His Pro Lys Ile Leu Ala Gln Val Gln Gln Glu Met			
305	310	315	320
Asp Ser Val Val Gly Arg Asp Arg Leu Ile Ala Glu Ala Asp Ile Pro			
325	330	335	
Asn Leu Thr Tyr Phe Gln Ala Val Ile Lys Glu Val Phe Arg Leu His			
340	345	350	
Pro Ser Thr Pro Leu Ser Leu Pro Arg Val Ala Asn Glu Ser Cys Glu			
355	360	365	
Ile Asn Gly Tyr His Ile Pro Lys Asn Thr Thr Leu Leu Val Asn Val			
370	375	380	
Trp Ala Ile Ala Arg Asp Pro Glu Val Trp Ala Asp Pro Leu Glu Phe			
385	390	395	400
Lys Pro Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn Val Asp Val			
405	410	415	
Lys Gly Asn Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile			
420	425	430	
Cys Ala Gly Leu Ser Leu Gly Leu Arg Met Val Gln Leu Met Thr Ala			
435	440	445	
Thr Leu Ala His Thr Tyr Asp Trp Ala Leu Ala Asp Gly Leu Met Pro			
450	455	460	
Glu Lys Leu Asn Met Asp Glu Ala Tyr Gly Leu Thr Leu Gln Arg Lys			
465	470	475	480
Val Pro Leu Asn Gly Pro Pro Asp Pro Val Gly Phe Ser Ala Arg Val			
485	490	495	

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 91..1629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAATTCCCC CCCCCCCCACA CCATTCATG CCTAAGTCCT CCATTTGCCG GCCTAATAAC 60

AAAAAGCCCCA CTCTTTCCGA CCATCTATAAC ATG CAA CAC CAA TAT TAT TCT TTA 114

Met Gln His Gln Tyr Tyr Ser Leu
1 5

ATT ACG ATG GAT GAT ATT AGC ATA ACC AGC TTA TTG GTG CCA TGT ACT 162
 Ile Thr Met Asp Asp Ile Ser Ile Thr Ser Leu Leu Val Pro Cys Thr
 10 15 20

TTT ATA TTA GGG TTC TTG CTT CTA TAT TCC TTC CTC AAC AAA AAA GTA 210
 Phe Ile Leu Gly Phe Leu Leu Leu Tyr Ser Phe Leu Asn Lys Lys Val
 25 30 35 40

AAG CCA CTG CCA CCT GGA CCG AAG CCA TGG CCC ATC GTC GGA AAT CTG 258
Lys Pro Leu Pro Pro Gly Pro Lys Pro Trp Pro Ile Val Gly Asn Leu
 45 50 55

CCA CAT CTT GGG CCG AAG CCC CAC CAG TCG ATG GCG GCG CTG GCA CGG 306

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Pro His Leu Gly Pro Lys Pro His Gln Ser Met Ala Ala Leu Ala Arg			
60	65	70	
 GTG CAC GGC CCA TTA ATT CAT CTG AAG ATG GGC TTT GTG CAT GTG GTT			354
Val His Gly Pro Leu Ile His Leu Lys Met Gly Phe Val His Val Val			
75	80	85	
 GTG GCC TCC TCA GCA TCC GTT GCG GAG AAA TTT CTG AAG GTG CAT GAC			402
Val Ala Ser Ser Ala Ser Val Ala Glu Lys Phe Leu Lys Val His Asp			
90	95	100	
 GCA AAC TTC TCG AGC AGG CCT CCC AAT TCG GGT GCA AAA CAC GTG GCC			450
Ala Asn Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala			
105	110	115	120
 TAC AAC TAT CAG GAC TTG GTC TTT GCT CCT TAT GGC CCA CGC TGG CGG			498
Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg			
125	130	135	
 ATG CTC AGG AAA ATC TGT GCA CTC CAC CTC TTC TCC GCC AAA GCC TTG			546
Met Leu Arg Lys Ile Cys Ala Leu His Leu Phe Ser Ala Lys Ala Leu			
140	145	150	
 AAC GAC TTC ACA CAC GTC AGA CAG GAT GAG GTG GGG ATC CTC ACT CGC			594
Asn Asp Phe Thr His Val Arg Gln Asp Glu Val Gly Ile Leu Thr Arg			
155	160	165	
 GTT CTA GCA GAT GCA GGA GAA ACG CCG TTG AAA TTA GGG CAG ATG ATG			642
Val Leu Ala Asp Ala Gly Glu Thr Pro Leu Lys Leu Gly Gln Met Met			
170	175	180	
 AAC ACA TGC GCC ACC AAT GCA ATA GCG CGT GTT ATG TTG GGT CGA CGC			690
Asn Thr Cys Ala Thr Asn Ala Ile Ala Arg Val Met Leu Gly Arg Arg			
185	190	195	200
 GTG GTT GGA CAC GCA GAC TCA AAG GCG GAG GAG TTT AAG GCA ATG GTA			738
Val Val Gly His Ala Asp Ser Lys Ala Glu Glu Phe Lys Ala Met Val			

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205 210 215

GTG GAG TTG ATG GTA TTA GCT GGT GTG TTC AAC TTA GGT GAT TTT ATC 786
 Val Glu Leu Met Val Leu Ala Gly Val Phe Asn Leu Gly Asp Phe Ile
 220 225 230

CCA CCT CTT GAA AAA TTG GAT CTT CAA GGT GTC ATT GCT AAG ATG AAG 834
 Pro Pro Leu Glu Lys Leu Asp Leu Gln Gly Val Ile Ala Lys Met Lys
 235 240 245

AAG CTT CAC TTG CGT TTC GAC TCG TTC TTG AGT AAG ATC CTT GGA GAC 882
Lys Leu His Leu Arg Phe Asp Ser Phe Leu Ser Lys Ile Leu Gly Asp
250 255 260

CAC AAG ATC AAC AGC TCA GAT GAA ACC AAA GGC CAT TCG GAT TTG TTG 930
 His Lys Ile Asn Ser Ser Asp Glu Thr Lys Gly His Ser Asp Leu Leu
 265 270 275 280

CTC ACC GAC GTA GAA ATT AAA GCG TTG CTC TTG AAC TTG TTT GCT GCA 1026
 Leu Thr Asp Val Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Ala Ala
 300 305 310

GGA ACT GAC ACA ACA TCA AGC ACT GTG GAA TGG TGC ATA GCT GAG TTA 1074
 Gly Thr Asp Thr Thr Ser Ser Thr Val Glu Trp Cys Ile Ala Glu Leu
 315 320 325

GTA CGA CAT CCT GAA ATC CTT GCC CAA GTC CAA AAA GAA CTC GAC TCT 1122
 Val Arg His Pro Glu Ile Leu Ala Gln Val Gln Lys Glu Leu Asp Ser
 320 325 330

GTT GTT GGT AAG AAT CGG GTG GTG AAG GAG GCT GAT CTG GCC GGA TTA 1170
Val Val Gly Lys Asn Arg Val Val Lys Glu Ala Asp Leu Ala Gly Leu
345 350 355 360

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CCA TTC CTC CAA GCG GTC GTC AAG GAA AAT TTC CGA CTC CAT CCC TCC	1218		
Pro Phe Leu Gln Ala Val Val Lys Glu Asn Phe Arg Leu His Pro Ser			
365	370	375	
ACC CCG CTC TCC CTA CCG AGG ATC GCA CAT GAG AGT TGT GAA GTG AAT	1266		
Thr Pro Leu Ser Leu Pro Arg Ile Ala His Glu Ser Cys Glu Val Asn			
380	385	390	
GGA TAC TTG ATT CCA AAG GGT TCG ACA CTT CTT GTC AAT GTT TGG GCA	1314		
Gly Tyr Leu Ile Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala			
395	400	405	
ATT GCT CGC GAT CCA AAT GTG TGG GAT GAA CCA CTA GAG TTC CGG CCT	1362		
Ile Ala Arg Asp Pro Asn Val Trp Asp Glu Pro Leu Glu Phe Arg Pro			
410	415	420	
GAA CGA TTC TTG AAG GGC GGG GAA AAG CCT AAT GTC GAT GTT AGA GGG	1410		
Glu Arg Phe Leu Lys Gly Gly Glu Lys Pro Asn Val Asp Val Arg Gly			
425	430	435	440
AAT GAT TTC GAA TTG ATA CCG TTC GGA GCG GGC CGA AGA ATT TGT GCA	1458		
Asn Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala			
445	450	455	
GGA ATG AGC TTA GGA ATA CGT ATG GTC CAG TTG TTG ACA GCA ACT TTG	1506		
Gly Met Ser Leu Gly Ile Arg Met Val Gln Leu Leu Thr Ala Thr Leu			
460	465	470	
AAC CAT GCG TTT GAC TTT GAT TTG GCG GAT GGA CAG TTG CCT GAA AGC	1554		
Asn His Ala Phe Asp Phe Asp Leu Ala Asp Gly Gln Leu Pro Glu Ser			
475	480	485	
TTA AAC ATG GAG GAA GCT TAT GGG CTG ACC TTG CAA CGA GCT GAC CCT	1602		
Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro			
490	495	500	
TTG GTA GTG CAC CCG AAG CCT AGG TAGGCACCTC ATGTTATCA AACCTAGGAC	1656		

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Leu Val Val His Pro Lys Pro Arg

505 510

TCATGTTTAG AGAACCTCTT GTTGTTTAT CAGATTGAAG TGTGATGTCC AAGAC

1711

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gln His Gln Tyr Tyr Ser Leu Ile Thr Met Asp Asp Ile Ser Ile

1 5 10 15

Thr Ser Leu Leu Val Pro Cys Thr Phe Ile Leu Gly Phe Leu Leu Leu

20 25 30

Tyr Ser Phe Leu Asn Lys Lys Val Lys Pro Leu Pro Pro Gly Pro Lys

35 40 45

Pro Trp Pro Ile Val Gly Asn Leu Pro His Leu Gly Pro Lys Pro His

50 55 60

Gln Ser Met Ala Ala Leu Ala Arg Val His Gly Pro Leu Ile His Leu

65 70 75 80

Lys Met Gly Phe Val His Val Val Ala Ser Ser Ala Ser Val Ala

85 90 95

Glu Lys Phe Leu Lys Val His Asp Ala Asn Phe Ser Ser Arg Pro Pro

100 105 110

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Asn Ser Gly Ala Lys His Val Ala Tyr Asn Tyr Gln Asp Leu Val Phe
115 120 125

Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu Arg Lys Ile Cys Ala Leu
130 135 140

His Leu Phe Ser Ala Lys Ala Leu Asn Asp Phe Thr His Val Arg Gln
145 150 155 160

Asp Glu Val Gly Ile Leu Thr Arg Val Leu Ala Asp Ala Gly Glu Thr
165 170 175

Pro Leu Lys Leu Gly Gln Met Met Asn Thr Cys Ala Thr Asn Ala Ile
180 185 190

Ala Arg Val Met Leu Gly Arg Arg Val Val Gly His Ala Asp Ser Lys
195 200 205

Ala Glu Glu Phe Lys Ala Met Val Val Glu Leu Met Val Leu Ala Gly
210 215 220

Val Phe Asn Leu Gly Asp Phe Ile Pro Pro Leu Glu Lys Leu Asp Leu
225 230 235 240

Gln Gly Val Ile Ala Lys Met Lys Lys Leu His Leu Arg Phe Asp Ser
245 250 255

Phe Leu Ser Lys Ile Leu Gly Asp His Lys Ile Asn Ser Ser Asp Glu
260 265 270

Thr Lys Gly His Ser Asp Leu Leu Asn Met Leu Ile Ser Leu Lys Asp
275 280 285

Ala Asp Asp Ala Glu Gly Arg Leu Thr Asp Val Glu Ile Lys Ala
290 295 300

Leu Leu Leu Asn Leu Phe Ala Ala Gly Thr Asp Thr Thr Ser Ser Thr

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305

310

315

320

Val Glu Trp Cys Ile Ala Glu Leu Val Arg His Pro Glu Ile Leu Ala

325

330

335

Gln Val Gln Lys Glu Leu Asp Ser Val Val Gly Lys Asn Arg Val Val

340

345

350

Lys Glu Ala Asp Leu Ala Gly Leu Pro Phe Leu Gln Ala Val Val Lys

355

360

365

Glu Asn Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu Pro Arg Ile

370

375

380

Ala His Glu Ser Cys Glu Val Asn Gly Tyr Leu Ile Pro Lys Gly Ser

385

390

395

400

Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp Pro Asn Val Trp

405

410

415

Asp Glu Pro Leu Glu Phe Arg Pro Glu Arg Phe Leu Lys Gly Gly Glu

420

425

430

Lys Pro Asn Val Asp Val Arg Gly Asn Asp Phe Glu Leu Ile Pro Phe

435

440

445

Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu Gly Ile Arg Met

450

455

460

Val Gln Leu Leu Thr Ala Thr Leu Asn His Ala Phe Asp Phe Asp Leu

465

470

475

480

Ala Asp Gly Gln Leu Pro Glu Ser Leu Asn Met Glu Glu Ala Tyr Gly

485

490

495

Leu Thr Leu Gln Arg Ala Asp Pro Leu Val Val His Pro Lys Pro Arg

500

505

510

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 971 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAT ATG CTT AGC ACT TTA ATC TCC CTT AAA GGA ACT GAT CTT GAC GGT	48
Asp Met Leu Ser Thr Leu Ile Ser Leu Lys Gly Thr Asp Leu Asp Gly	
1 5 10 15	
GAC GGA GGA AGC TTA ACG GAT ACT GAG ATT AAA GCC TTG CTA TTG AAC	96
Asp Gly Gly Ser Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Asn	
20 25 30	
ATG TTC ACA GCT GGA ACT GAC ACG TCA GCA AGT ACG GTG GAC TGG GCT	144
Met Phe Thr Ala Gly Thr Asp Thr Ser Ala Ser Thr Val Asp Trp Ala	
35 40 45	
ATA GCT GAA CTT ATC CGT CAC CCG GAT ATA ATG GTT AAA GCC CAA GAA	192
Ile Ala Glu Leu Ile Arg His Pro Asp Ile Met Val Lys Ala Gln Glu	
50 55 60	
GAA CTT GAT ATT GTT GTG GGC CGT GAC AGG CCT GTT AAT GAA TCA GAC	240
Glu Leu Asp Ile Val Val Gly Arg Asp Arg Pro Val Asn Glu S r Asp	
65 70 75 80	

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ATC GCT CAG CTT CCT TAC CTT CAG GCG GTT ATC AAA GAG AAT TTC AGG		288
Ile Ala Gln Leu Pro Tyr Leu Gln Ala Val Ile Lys Glu Asn Phe Arg		
85	90	95
CTT CAT CCA CCA ACA CCA CTC TCG TTA CCA CAC ATC GCG TCA GAG AGC		336
Leu His Pro Pro Thr Pro Leu Ser Leu Pro His Ile Ala Ser Glu Ser		
100	105	110
TGT GAG ATC AAC GGC TAC CAT ATC CCG AAA GGA TCG ACT CTA TTT GAC		384
Cys Glu Ile Asn Gly Tyr His Ile Pro Lys Gly Ser Thr Leu Phe Asp		
115	120	125
GGA CAT ATG GGC CTA GGC CGT GAC CCG GAT CAA TGG TCC GAC CCG TTA		432
Gly His Met Gly Leu Gly Arg Asp Pro Asp Gln Trp Ser Asp Pro Leu		
130	135	140
GCA TTT AAA CCC GAG AGA TTC TTA CCC GGT GGT GAA AAA TCC GGC GTT		480
Ala Phe Lys Pro Glu Arg Phe Leu Pro Gly Gly Glu Lys Ser Gly Val		
145	150	155
GAT GTG AAA GGA AGC GAT TTC GAG CTA ATA CCG TTC GGG GCT GGG AGG		528
Asp Val Lys Gly Ser Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg		
165	170	175
CCA ATC TGT GCA GGT TTA AGT TTA GGG CTA CGT ACA GAT TTA AGT TGC		576
Pro Ile Cys Ala Gly Leu Ser Leu Gly Leu Arg Thr Asp Leu Ser Cys		
180	185	190
CTT CAC GCC AAC GTT GCT CAC AAG CAT TTG ATT GGG AAC TTC AGC TGG		624
Leu His Ala Asn Val Ala His Lys His Leu Ile Gly Asn Phe Ser Trp		
195	200	205
AGA AGT TAC GCC GGA CAA CCT GAA TAT CGC AGG AAA AGT TTA CTG GGC		672
Arg Ser Tyr Ala Gly Gln Pro Glu Tyr Arg Arg Lys Ser Leu Leu Gly		
210	215	220
TTT ACA CTG CAA AGA GCG GTT CCT TCG GTG GTA CAC CCT AAG CCA AGG		720

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Phe Thr Leu Gln Arg Ala Val Pro Ser Val Val His Pro Lys Pro Arg				
225	230	235	240	
TTG GCC CCG AAC GTT TAT GGA CCC CGG GTC GGC TTA AAA TTT AAC TTT				768
Leu Ala Pro Asn Val Tyr Gly Pro Arg Val Gly Leu Lys Phe Asn Phe				
245	250	255		
GCT TCT TGG ACA AGG TAT ATG GCT TGC ACG AAA CTA ACG TTT T				811
Ala Ser Trp Thr Arg Tyr Met Ala Cys Thr Lys Leu Thr Phe				
260	265	270		
AACACACCGT AGTTTGATCC GGAGTTAGCT TTATGTAAGA ACGTGTAAACG CCAAATCAAG				871
CCATTATCAA CTACCGTGAG CTGTTTGAC CCTATCTATA AATCTTGAAG AGGAACATTT				931
CAGAACTCTT GACTATGTTT CAGGAACAAA AAAAAAAA				971

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Met Leu Ser Thr Leu Ile Ser Leu Lys Gly Thr Asp Leu Asp Gly			
1	5	10	15

Asp Gly Gly Ser Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn			
20	25	30	

Met Phe Thr Ala Gly Thr Asp Thr Ser Ala Ser Thr Val Asp Trp Ala			
35	40	45	

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Ile Ala Glu Leu Ile Arg His Pro Asp Ile Met Val Lys Ala Gln Glu
50 55 60

Glu Leu Asp Ile Val Val Gly Arg Asp Arg Pro Val Asn Glu Ser Asp
65 70 75 80

Ile Ala Gln Leu Pro Tyr Leu Gln Ala Val Ile Lys Glu Asn Phe Arg
85 90 95

Leu His Pro Pro Thr Pro Leu Ser Leu Pro His Ile Ala Ser Glu Ser
100 105 110

Cys Glu Ile Asn Gly Tyr His Ile Pro Lys Gly Ser Thr Leu Phe Asp
115 120 125

Gly His Met Gly Leu Gly Arg Asp Pro Asp Gln Trp Ser Asp Pro Leu
130 135 140

Ala Phe Lys Pro Glu Arg Phe Leu Pro Gly Gly Glu Lys Ser Gly Val
145 150 155 160

Asp Val Lys Gly Ser Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg
165 170 175

Pro Ile Cys Ala Gly Leu Ser Leu Gly Leu Arg Thr Asp Leu Ser Cys
180 185 190

Leu His Ala Asn Val Ala His Lys His Leu Ile Gly Asn Phe Ser Trp
195 200 205

Arg Ser Tyr Ala Gly Gln Pro Glu Tyr Arg Arg Lys Ser Leu Leu Gly
210 215 220

Phe Thr Leu Gln Arg Ala Val Pro Ser Val Val His Pro Lys Pro Arg
225 230 235 240

Leu Ala Pro Asn Val Tyr Gly Pro Arg Val Gly L u Lys Phe Asn Phe

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245

250

255

Ala Ser Trp Thr Arg Tyr Met Ala Cys Thr Lys Leu Thr Phe

260

265

270

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1478..1927

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2651..3091

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3170..3340

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3421..3900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCGACTCTC TCCCTTCGC TTGCTACTTT TTCTACATAA ATAAATGCAA TGATAAATT

60

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GTGCACACAT TCGTATGTTT GAAACATGGT AGGATCCACA ATTTATACTT TATAGACTCA	120
AAATGGAAAA GAAACGTACA TTATAAATT ATCTGCAATT TGTTTCTCT TGCTAAACTA	180
GACTGTATAA TAACCTCTGT ATATGCTATT ACTCGATTGT AAACGTACCC CGCAAGTCGC	240
AAGCAAGGTA AATAAAGTAT AATTATATT TCACACACGA AACTTTAATT ATTATTTTA	300
TCACTTGCAG ATTAACAGTA AAAAAAAAAA AAATGTGACT TTAACGGCGA CAAAAACTAC	360
TGATCTTCT CCAATATTAA AATAATATAA TTAATAAACG TCTTTCATA CTTGTATTT	420
CCGACCCGAG TTCTGAAAGT GAAAACATAT GGTACTAGAT ATTCTCGATT TGTTTGTAG	480
CCACTAGACT CTAAACAGAA AAAAGAAGCC AAAAGGACAA CGTTAAAAAA GAGACACTGT	540
TATTAAAAGT TAGAAACCAA ACGGTGAAAA TCCAGCTACA TACATAAAAT AAAGCCAAGG	600
TACCAAACTA ATGAACGTGA ACCTCTTTT TCTTTCTTT TTTGTTAAAG GATTTATGAA	660
CTGTAACCTA GAATGCTTGG TTTGTGGCA GTGTAATATA TGACACACAT GCATTTTTT	720
TGTTTGTCAA ATAGGAAGAC TTCTTTTTC TTTATCAACT TCCTTATTTT CATAAAACAA	780
AACACTGAAA AAAGTACAGA TGTTCTCACG TACGTCACGT GTACATACAT ATATATTAGA	840
CCACTATATA ATAAGATATG AAGTGTAGG TTTAAATCAA TTAACGAATC CCATCCAAAT	900
GATGAAACAG TTAACAAGAA ATCAAAATAG TTTATTAGGG TTACAATGAT TTTATACTTT	960
TAAGAAATCT TAGAACCTAT CACTTACAAA TGAGTAAATG ACCATTACTC CTCGAGAAC	1020
TAAGGCGCTT AAGGAAGCAT TCGAATCGG GTGTGAAAAA GATCTATTTT TTGAATTATT	1080
TCACACAATT TCTTAATGTC AATTTCGAT GCTCCATAT TCTCCACGGT TTAAAGCAAG	1140
ATTGGTGGGA AAGGGATATT CTCGCATCGA TTACAATGAA ATATGGTTG AAAAAAAAAA	1200

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AAAAAAAATTA CTCAATGTTG CACCAAAAC CAGAAAACTC TAAGTTGC	GC	TAATAAAAAA	1260
AAAAGTTATA AACCCAACAT CAAACCAAAA CCGTACTAAA CTGTCCCATA	TGAGATTAG		1320
CTTTAAATAA ATTAGTACTT CTCATAACGA TAACTAAATT AAATTTCCCT AGCCAAGACA			1380
TACATATAGT TTTGATTGAC AAAAAAAA AAAACTCCTC TATTTATAGC TTGTGTTTG			1440
TTTCCTCATT TTTCACTTAC CATTCAAACC CAACACT ATG GCA ACT CTA TTT CTC			1495
	Met Ala Thr Leu Phe Leu		
	1	5	
ACA ATC CTC CTA GCC ACT GTC CTC TTC CTC ATC CTC CGT ATC TTC TCT			1543
Thr Ile Leu Leu Ala Thr Val Leu Phe Leu Ile Leu Arg Ile Phe Ser			
10	15	20	
CAC CGT CGC AAC CGC AGC CAC AAC AAC CGT CTT CCA CCG GGG CCA AAC			1591
His Arg Arg Asn Arg Ser His Asn Asn Arg Leu Pro Pro Gly Pro Asn			
25	30	35	
CCA TGG CCC ATC ATC GGA AAC CTC CCT CAC ATG GGC ACT AAG CCT CAT			1639
Pro Trp Pro Ile Ile Gly Asn Leu Pro His Met Gly Thr Lys Pro His			
40	45	50	
CGA ACC CTT TCC GCC ATG GTT ACT ACT TAC GGC CCT ATC CTC CAC CTC			1687
Arg Thr Leu Ser Ala Met Val Thr Thr Tyr Gly Pro Ile Leu His Leu			
55	60	65	70
CGA CTA GGG TTC GTA GAC GTC GTG GTC GCC GCT TCT AAA TCC GTG GCC			1735
Arg Leu Gly Phe Val Asp Val Val Val Ala Ala Ser Lys Ser Val Ala			
75	80	85	
GAG CAG TTC TTG AAA ATA CAC GAC GCC AAT TTC GCT AGC CGA CCA CCA			1783
Glu Gln Phe Leu Lys Ile His Asp Ala Asn Phe Ala Ser Arg Pro Pro			
90	95	100	
AAC TCA GGA GCC AAA CAC ATG GCA TAT AAC TAT CAA GAT CTT GTC TTT			1831

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Asn Ser Gly Ala Lys His Met Ala Tyr Asn Tyr Gln Asp Leu Val Phe

105

110

115

GCA CCT TAC GGA CAC CGA TGG AGA CTG TTG AGA AAG ATT AGT TCT GTT 1879
 Ala Pro Tyr Gly His Arg Trp Arg Leu Leu Arg Lys Ile Ser Ser Val
 120 125 130

CAT CTA TTT TCA GCT AAA GCT CTC GAA GAT TTC AAA CAT GTT CGA CAG 1927
 His Leu Phe Ser Ala Lys Ala Leu Glu Asp Phe Lys His Val Arg Gln
 135 140 145 150

GTAAAAACAAT TATAAACGGT ATTCTCATTT TCTAACGCTA TAGCTCACTG GCCTGTAATC 1987

ATGTCATTTC AATGTTTGATCTTTCTTT ATATATACAT AATTATAATT TATAATTGGG 2047

ATTTCAAACC CTATCTCTCA CTATTTCAAG ACTAGACCGG ATTGGAATTGAACTTTGT 2107

AATGAATATT AGTATCTGCA CATAAATTTT ATGTTAAAGT TGGGTTTCT TAAAGTGAAT 2167

TTATATATTA AAAATATATA AACGATTGGG TTTTACTCAA ATGAATTAC ATAAGAGCTA 2227

GGTATAAGTG CAAATATGCA ATACTGTCAT TGCGTGGAT GTATAAAAGT ATGATCTAAC 2287

TTTGATGATG CCATGGAAA ATTGGAAAGT TCAGATCCAG AGGAAACATT GCTTGAATTA 2347

TAAAATGTAT GGACCACATT GTTCCCTAA ATGGAAGGTC TCACGAGTTT CTCAATTCA 2407

GACTACTGAT AATATATGCT ATTATAGATT TTATTTCTG ATTATTTTT TTGGTTTAAT 2467

TTAATTAGAG TAAATTTTA AAAAGAAATA TATGGTTTG TTAACCGTGT TTTAAAATTG 2527

GATAGAGCTT TTAGATCATA ATCATAATTT TTTCGTATTA ATTGTGATTA TGTTGGACGA 2587

AAATACTTAA TTAGTATTCA AGAAAACCTCT TATTCTAAAA ACAGAAATAA ATGAATTAA 2647

CAG GAA GAG GTT GGA ACG CTA ACG CGG GAG CTA GTG CGT GTT GGC ACG 2695
 Glu Glu Val Gly Thr Leu Thr Arg Glu Leu Val Arg Val Gly Thr

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1	5	10	15	
				2743
AAA CCC GTG AAT TTA GGC CAG TTG GTG AAC ATG TGT GTA GTC AAC GCT Lys Pro Val Asn Leu Gly Gln Leu Val Asn Met Cys Val Val Asn Ala				
20		25		30
				2791
CTA GGA CGA GAG ATG ATC GGA CGG CGA CTG TTC GGC GCC GAC GCC GAT Leu Gly Arg Glu Met Ile Gly Arg Arg Leu Phe Gly Ala Asp Ala Asp				
35		40		45
				2839
CAT AAA GCT GAC GAG TTT CGA TCG ATG GTG ACG GAA ATG ATG GCT CTC His Lys Ala Asp Glu Phe Arg Ser Met Val Thr Glu Met Met Ala Leu				
50		55		60
				2887
GCC GGA GTA TTT AAC ATC GGA GAT TTC GTG CCG TCA CTT GAT TGG TTA Ala Gly Val Phe Asn Ile Gly Asp Phe Val Pro Ser Leu Asp Trp Leu				
65		70		75
				2935
GAT TTA CAA GGC GTC GCT GGT AAA ATG AAA CGG CTT CAC AAA AGA TTC Asp Leu Gln Gly Val Ala Gly Lys Met Lys Arg Leu His Lys Arg Phe				
80		85		95
				2983
GAC GCT TTT CTA TCG TCG ATT TTG AAA GAG CAC GAA ATG AAC GGT CAA Asp Ala Phe Leu Ser Ser Ile Leu Lys Glu His Met Asn Gly Gln				
100		105		110
				3031
GAT CAA AAG CAT ACA GAT ATG CTT AGC ACT TTA ATC TCC CTT AAA GGA Asp Gln Lys His Thr Asp Met Leu Ser Thr Leu Ile Ser Leu Lys Gly				
115		120		125
				3079
ACT GAT CTT GAC GGT GAC GGA GGA AGC TTA ACG GAT ACT GAG ATT AAA Thr Asp Leu Asp Gly Asp Gly Ser Leu Thr Asp Thr Glu Ile Lys				
130		135		140
				3131
GCC TTG CTA TTG GTCAGTTTT TGACAATTAA TTTCCTTAAA AATCGTATAT Ala Leu Leu Leu				

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AATGAAAGTT AGATTGTTT TTTGGTTGT AAATACAG AAC ATG TTC ACA GCT	3184	
Asn Met Phe Thr Ala		
1	5	
GGA ACT GAC ACG TCA GCA AGT ACG GTG GAC TGC GCT ATA GCT GAA CTT	3232	
Gly Thr Asp Thr Ser Ala Ser Thr Val Asp Trp Ala Ile Ala Glu Leu		
10	15	20
ATC CGT CAC CCG GAT ATA ATG GTT AAA GCC CAA GAA GAA CTT GAT ATT	3280	
Ile Arg His Pro Asp Ile Met Val Lys Ala Gln Glu Glu Leu Asp Ile		
25	30	35
GTT GTG GGC CGT GAC AGG CCT GTT AAT GAA TCA GAC ATC GCT CAG CTT.	3328	
Val Val Gly Arg Asp Arg Pro Val Asn Glu Ser Asp Ile Ala Gln Leu		
40	45	50
CCT TAC CTT CAG GTACCGTTAA CCCAACCGG AATTTGGAAT TGTTTTGGTT	3380	
Pro Tyr Leu Gln		
55		
AGCGAGCTAT TGTTGTTAAT CCGGTTTG G TTTAAACAG GCG GTT ATC AAA GAG	3435	
Ala Val Ile Lys Glu		
1	5	
AAT TTC AGG CTT CAT CCA CCA ACA CCA CTC TCG TTA CCA CAC ATC GCG	3483	
Asn Phe Arg Leu His Pro Pro Thr Pro Leu Ser Leu Pro His Ile Ala		
10	15	20
TCA GAG AGC TGT GAG ATC AAC GGC TAC CAT ATC CCG AAA GGA TCG ACT	3531	
Ser Glu Ser Cys Glu Ile Asn Gly Tyr His Ile Pro Lys Gly Ser Thr		
25	30	35
CTA TTG ACG AAC ATA TGG GCC ATA GCC CGT GAC CCG GAT CAA TGG TCC	3579	
Leu Leu Thr Asn Ile Trp Ala Ile Ala Arg Asp Pro Asp Gln Trp Ser		
40	45	50
GAC CCG TTA GCA TTT AAA CCC GAG AGA TTC TTA CCC GGT GGT GAA AAA	3627	

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Asp Pro Leu Ala Phe Lys Pro Glu Arg Phe Leu Pro Gly Gly Glu Lys
 55 60 65

TCC GGC GTT GAT GTG AAA GGA AGC GAT TTC GAG CTA ATA CCG TTC GGA 3675
 Ser Gly Val Asp Val Lys Gly Ser Asp Phe Glu Leu Ile Pro Phe Gly
 70 75 80 85

GCT GGG AGG AGA ATC TGT GCC GGT TTA AGT TTA GGG TTA CGT ACG ATT 3723
 Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Leu Gly Leu Arg Thr Ile
 90 95 100

CAG TTT CTT ACG GCG ACG TTG GTT CAA GGA TTT GAT TGG GAA TTA GCT 3771
 Gln Phe Leu Thr Ala Thr Leu Val Gln Gly Phe Asp Trp Glu Leu Ala
 105 110 115

GGA GGA GTT ACG CCG GAG AAG CTG AAT ATG GAG GAG AGT TAT GGG CTT 3819
 Gly Gly Val Thr Pro Glu Lys Leu Asn Met Glu Glu Ser Tyr Gly Leu
 120 125 130

ACA CTG CAA AGA GCG GTT CCT TTG GTG GTA CAT CCT AAG CCA AGG TTG 3867
 Thr Leu Gln Arg Ala Val Pro Leu Val Val His Pro Lys Pro Arg Leu
 135 140 145

GCT CCG AAC GTT TAT GGA CTC GGG TCG GGT TAAAATTTAA CTTTGCTTCT 3917
 Ala Pro Asn Val Tyr Gly Leu Gly Ser Gly
 150 155 160

TGGACAAGGT ATATGGCTTG CACGAAAATA AAGTTTTAAA ACAGCGTAGT TTGATCCGGA 3977

GTTAGCTTAA TGTAAGAACG TGTAACGCCA AATCAAGTCA TTATTAAATA TTGTGAGTTG 4037

TTTGTAAACCT ATATATAAAAT CTTGAAGAGG AAGATTCAG AAATCTTGAA TATGTTTTAG 4097

GAAAAACATT GTTTTTTTA CAGTAGCGCA AGTTGAATTA AAACCTATTC CTTACAGAAC 4157

CAAATGCATT AATAATTCTA GATATTTTG GCCAAGACAA TCAGATTTT CAATATTC 4217

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TATATACTAG GTGGAACACC ACCACCTGCA ACTCTGCAAC ACATGTTACG TTACACAATC	4277
ACTTTGGCG GTTTCAATT ATTTATATAA AATTGTAAAT GTTTGTACAC AGTAGAAAAT	4337
TAGTAATAGT GAATTTGTT TCTCCGAATA TGTATAGCAA TATATATGGC ATGGATCAA	4397
CTAGCCGACA TCCTAACATTG TTCACAGCTT TCCTTTTAC TTATCTAGTC GATTAAGCAT	4457
CAGAAAGTAT GTTTAATT TTAAATTGAA AAAAGGTGTA CTTACAAGTT CGGGTGTCA	4517
CACGGAGGAG AGCTACAATA ATGAAAAGC TGACTCAAGA AGGGCTATAG AAGAAACAAG	4577
AGTCACGGAA CAAGTTGTCA CTCTCAATCT CCAGTACACT AGCTTCCATA ACTCTCTCTC	4637
TTTCTCTCTT TCTTCTCTCT CTAAAAGTTA TCAGAATAGA AATCTCTCTC TCTCAACAAG	4697
TCTAACAGTG CCATTTGTAT CTCTGAACTC CAACATGGCT CCTCTGGTTC TCTACCTTCT	4757
CACTCTCCTC ATGGCTGGCC ATTCCAGTAA GAACTCTCAC TGATCTTCTT CACCTTGTT	4817
TATGGATTTG GTCTCTCAGT CTCACTCTCG CTTACCCCTT CACATTCAAGC TCTGGCTCTC	4877
TGGTTTAAGA AACCTTAAT CTACAAAGCT TGCTTCTCTC GCAAATGAAC TACCTTACTT	4937
ATCTCTTATG CAACTCTGT TGATGATTTG CAAACATCTT AACCTCTCGA AACAAAGATT	4997
ACAAATCTTA CTGGCTTCAC TTACAATT TTCCCATT TTTCTTCTT TGTTAGGTGC	5057
CTCATGGTGT GTGTGCAAAA CAGGGCTGAG TGACTCAGTG CTACAAAAGA CATTAGACTA	5117
TGCTTGTGGA AATGGAGCTG ACTGTAACCC AACTCACCCA AAAGGCTCTT GCTTCAATCC	5177
TGACAATGTT AGGGCTCATT GCAACTATGC AGTCAATAGC TTCTTCCAAA AGAAAGGTCA	5237
AGCTTCTGAG TCTTGTAACT TCACTGGTAC TGCCACTCTT ACCACCACCG ATCCCAGTAA	5297
GTTTTCAGAA TGTTAACACT CTTGTGATCT TTAGAACCT ACAAAATT TTAGTCTCAGA	5357

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AAGTTCAAGT TCAAGGTCTT TTGGTTAGAG TACTAAAGAT TCAAGTAGAG ACTAGGCGTG	5417
AGATATTTTT TCTCTGATGT GTGATTTTTT GGCACAGGCT ATACAGGATG TGCATTCCCT	5477
TCTAGTGCTA GGTACGGCTC TTTGCTTCTC TACACATTAA TTTTCTTAAT GGCTTTATCT	5537
AGAACTTTGA AGGATACCAT TTTATTTTTT TTGGACAAAG AAGGATAGCC ATTTAATACT	5597
ACACTTTAAT GTTGGATTAA CTAACTTATT ATGCCTATT AATGGCCTAC ACTTTAAGTG	5657
GACACAAGCT TGATTTGGTT ATAAAAAAAG TGCACTATAA TCTTATTTA CTGAACCCTT	5717
TTTTCTATGA TTTTTTACT AAACTTAGA TAACATCTAC ACAATTCAA TTGCCTTTT	5777
TTGGGGATTG TATAAGTTTG AACCTATGGT TAGTGTATTG ACTTGCGCGT CTCTTATTGC	5837
AACGGTTCTT TGAAAACACA TTAATGATAA ATAAATTGAA AAGTATAGAG ATGGCAATTG	5897
TTTCAAAAGC TAATCTTTCT GCTTGCTAAT ACTTTACATA AAAAACAAAA AATTAAGAAG	5957
ATTTTCAAAC AATACAACCTT TTTTACCTTG TCCTAACAAA TTCAACTCAA ATGACATGTG	6017
TTTGCTTTAA AATAGTAACA ACTGTAAATT CATTGCTCT TGAGACATAA GTGCAAGCTA	6077
AAGATAAACG CAAGCAATAC AATTAGGCCT AATTAAGATT ACGAATATTG TTGTTTGT	6137
ATAGTGGTTC TAGTGGAAAGC GGTAGCACCA CCGTGACGCC AGGCAAAAC AGTCCAAAAG	6197
GAAGCAACAG CATCACCAACA TTTCCCGGCG GAAACAGTCC ATACACTGGC ACACCATCCA	6257
CCGGATTATT AGGAGGCAAT ATCACTGATG CAACTGGAAC CGGGTTGAAC CGGGATTACT	6317
CAACCGAAAG CAGTGGATTG GCGCTCTATT ACTCCAACAA CCTTCTGTTA ACCGGCTTT	6377
GTTCTCTCGT GATGATGCTC TGAAGAAGAA TCACCGTCTT CTTTTAGTTT ATGCTTAGTC	6437
AAAAAAATAT GTTATTTATA TGTCTTGTT GTTTAGAGA TAATTAATC TGGATTCGG	6497

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TTCTTTTTA CTTTCCGGTT TTAAGAAAAC AATTATCAAT GTAAAACCAA ATCTACTATC 6557

GATCGGTTTG GTACGAATTC CTGCAGCCCG GGGGATCC 6595

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Thr Leu Phe Leu Thr Ile Leu Leu Ala Thr Val Leu Phe Leu
1 5 10 15

Ile Leu Arg Ile Phe Ser His Arg Arg Asn Arg Ser His Asn Asn Arg
20 25 30

Leu Pro Pro Gly Pro Asn Pro Trp Pro Ile Ile Gly Asn Leu Pro His
35 40 45

Met Gly Thr Lys Pro His Arg Thr Leu Ser Ala Met Val Thr Thr Tyr
50 55 60

Gly Pro Ile Leu His Leu Arg Leu Gly Phe Val Asp Val Val Val Ala
65 70 75 80

Ala Ser Lys Ser Val Ala Glu Gln Phe Leu Lys Ile His Asp Ala Asn
85 90 95

Phe Ala Ser Arg Pro Pro Asn Ser Gly Ala Lys His Met Ala Tyr Asn
100 105 110

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Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly His Arg Trp Arg Leu Leu
115 120 125

Arg Lys Ile Ser Ser Val His Leu Phe Ser Ala Lys Ala Leu Glu Asp
130 135 140

Phe Lys His Val Arg Gln
145 150

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Glu Glu Val Gly Thr Leu Thr Arg Glu Leu Val Arg Val Gly Thr Lys
1 5 10 15

Pro Val Asn Leu Gly Gln Leu Val Asn Met Cys Val Val Asn Ala Leu
20 25 30

Gly Arg Glu Met Ile Gly Arg Arg Leu Phe Gly Ala Asp Ala Asp His
35 40 45

Lys Ala Asp Glu Phe Arg Ser Met Val Thr Glu Met Met Ala Leu Ala
50 55 60

Gly Val Phe Asn Ile Gly Asp Phe Val Pro Ser Leu Asp Trp Leu Asp
65 70 75 80

Leu Gln Gly Val Ala Gly Lys Met Lys Arg Leu His Lys Arg Phe Asp

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85

90

95

Ala Phe Leu Ser Ser Ile Leu Lys Glu His Glu Met Asn Gly Gln Asp

100

105

110

Gln Lys His Thr Asp Met Leu Ser Thr Leu Ile Ser Leu Lys Gly Thr

115

120

125

Asp Leu Asp Gly Asp Gly Ser Leu Thr Asp Thr Glu Ile Lys Ala

130

135

140

Leu Leu Leu

145

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asn Met Phe Thr Ala Gly Thr Asp Thr Ser Ala Ser Thr Val Asp Trp

1

5

10

15

Ala Ile Ala Glu Leu Ile Arg His Pro Asp Ile Met Val Lys Ala Gln

20

25

30

Glu Glu Leu Asp Ile Val Val Gly Arg Asp Arg Pro Val Asn Glu Ser

35

40

45

Asp Ile Ala Gln Leu Pro Tyr Leu Gln

50

55

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala Val Ile Lys Glu Asn Phe Arg Leu His Pro Pro Thr Pro Leu Ser

1 5 10 15

Leu Pro His Ile Ala Ser Glu Ser Cys Glu Ile Asn Gly Tyr His Ile

20 25 30

Pro Lys Gly Ser Thr Leu Leu Thr Asn Ile Trp Ala Ile Ala Arg Asp

35 40 45

Pro Asp Gln Trp Ser Asp Pro Leu Ala Phe Lys Pro Glu Arg Phe Leu

50 55 60

Pro Gly Gly Glu Lys Ser Gly Val Asp Val Lys Gly Ser Asp Phe Glu

65 70 75 80

Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Leu

85 90 95

Gly Leu Arg Thr Ile Gln Phe Leu Thr Ala Thr Leu Val Gln Gly Phe

100 105 110

Asp Trp Glu Leu Ala Gly Gly Val Thr Pro Glu Lys Leu Asn Met Glu

115 120 125

Glu Ser Tyr Gly Leu Thr Leu Gln Arg Ala Val Pro Leu Val Val His

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130 135 140

Pro Lys Pro Arg Leu Ala Pro Asn Val Tyr Gly Leu Gly Ser Gly

145 150 155

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 22..1563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGTCGAGAAA GAAGAACAGC C ATG TTT CTC ATA GTA GTG ATC ACC TTC CTC 51

Met Phe Leu Ile Val Val Ile Thr Phe Leu

1 5 10

TTC GCC GTG TTT TTG TTC CGG CTT TCC TCC GGC AAA TCC CAA CGC 99

Phe Ala Val Phe Leu Phe Arg Leu Leu Phe Ser Gly Lys Ser Gln Arg

15 20 25

CAC TCG CTC CCT CTC CCT CCT GGC CCC AAA CCA TGG CCG GTG GTT GGC 147

His Ser Leu Pro Leu Pro Pro Gly Pro Lys Pro Trp Pro Val Val Gly

30 35 40

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AAC TTA CCT CAC TTG GGC CCC TTC CCG CAC CAC TCC ATC GCG GAG TTG			195
Asn Leu Pro His Leu Gly Pro Phe Pro His His Ser Ile Ala Glu Leu			
45	50	55	
 GCG AAG AAA CAC GGG CCG CTC ATG CAC CTC CGC CTC GGC TAC GTT GAC			243
Ala Lys Lys His Gly Pro Leu Met His Leu Arg Leu Gly Tyr Val Asp			
60	65	70	
 GTA GTC GTG GCG GCA TCA GCA TCC GTA GCG GCC CAG TTC TTG AAG ACT			291
Val Val Val Ala Ala Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Thr			
75	80	85	90
 CAC GAC GCC AAT TTC TCC AGC CGA CCG CCC AAC TCC GGC GCC AAG CAC			339
His Asp Ala Asn Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His			
95	100	105	
 CTC GCC TAT AAC TAC CAG GAC CTC GTG TTC AGG CCG TAC GGT CCA CGG			387
Leu Ala Tyr Asn Tyr Gln Asp Leu Val Phe Arg Pro Tyr Gly Pro Arg			
110	115	120	
 TGG CGC ATG TTC CGG AAG ATC AGC TCC GTC CAT CTG TTC TCC GGC AAA			435
Trp Arg Met Phe Arg Lys Ile Ser Ser Val His Leu Phe Ser Gly Lys			
125	130	135	
 GCC TTG GAT GAT CTT AAA CAC GTC CGG CAG GAG GAG GTA AGT GTG CTA			483
Ala Leu Asp Asp Leu Lys His Val Arg Gln Glu Glu Val Ser Val Leu			
140	145	150	
 GCG CAT GCC TTG GCA AAT TCA GGG TCA AAG GTA GTG AAC CTG GCG CAA			531
Ala His Ala Leu Ala Asn Ser Gly Ser Lys Val Val Asn Leu Ala Gln			
155	160	165	170
 CTG CTG AAC CTG TGC ACG GTC AAT GCT CTA GGA AGG GTG ATG GTA GGG			579
Leu Leu Asn Leu Cys Thr Val Asn Ala Leu Gly Arg Val Met Val Gly			
175	180	185	
 CGG AGG GTT TTC GGC GAC GGC GGA GGC GAC GAT CCG AAG GCG GAC			627

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Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Asp Asp Pro Lys Ala Asp			
190	195	200	
GAG TTC AAA TCG ATG GTG GTG GAG ATG ATG GTG TTG GCA GGA GTG TTC			675
Glu Phe Lys Ser Met Val Val Glu Met Met Val Leu Ala Gly Val Phe			
205	210	215	
AAC ATA GGT GAC TTC ATC CCC TCT CTC GAA TGG CTT GAC TTG CAA GGC			723
Asn Ile Gly Asp Phe Ile Pro Ser Leu Glu Trp Leu Asp Leu Gln Gly			
220	225	230	
GTG GCG TCC AAG ATG AAG AAG CTC CAC AAG AGA TTC GAC GAC TTC TTG			771
Val Ala Ser Lys Met Lys Lys Leu His Lys Arg Phe Asp Asp Phe Leu			
235	240	245	250
ACA GCC ATT GTC GAG GAC CAC AAG AAG GGC TCC GGC ACG GCG GGG CAC			819
Thr Ala Ile Val Glu Asp His Lys Lys Gly Ser Gly Thr Ala Gly His			
255	260	265	
GTC GAC ATG TTG ACC ACT CTG CTC TCG CTC AAG GAA GAC GCC GAC GGC			867
Val Asp Met Leu Thr Thr Leu Leu Ser Leu Lys Glu Asp Ala Asp Gly			
270	275	280	
GAA GGA GGC AAG CTC ACC GAT ACT GAA ATC AAA GCT TTG CTT TTG AAC			915
Glu Gly Lys Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn			
285	290	295	
ATG TTC ACG GCT GGC ACT GAT ACG TCA TCG AGC ACG GTG GAA TGG GCA			963
Met Phe Thr Ala Gly Thr Asp Thr Ser Ser Ser Thr Val Glu Trp Ala			
300	305	310	
ATA GCT GAA CTC ATT CGG CAC CCT CAT ATG CTA GCG CGA GTT CAG AAA			1011
Ile Ala Glu Leu Ile Arg His Pro His Met Leu Ala Arg Val Gln Lys			
315	320	325	330
GAG CTT GAC GAT TTT GTT GGC CAT GAC CGA CTT GTG ACC GAA TCC GAC			1059
Glu Leu Asp Asp Phe Val Gly His Asp Arg Leu Val Thr Glu Ser Asp			

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		340		345
CCT TAC CTC CAA GCC GTG ATC AAG GAA ACG TTC CGA				1107
Pro Tyr Leu Gln Ala Val Ile Lys Glu Thr Phe Arg				
	355		360	
ACT CCT CTC TCG TTG CCT CGT ATG GCA GCC GAG AGT				1155
Thr Pro Leu Ser Leu Pro Arg Met Ala Ala Glu Ser				
	370		375	
GGG TAC CAC ATC CCG AAA GGC TCC ACA CTC TTG GTC				1203
Gly Tyr His Ile Pro Lys Gly Ser Thr Leu Leu Val				
	385		390	
ATA TCG CGT GAC CCG GCT GAA TGG GCC GAC CCA CTG				1251
Ile Ser Arg Asp Pro Ala Glu Trp Ala Asp Pro Leu				
	400		405	410
GAG AGG TTC CTG CCG GGG GGC GAA AAG CCT AAT GTT				1299
Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn Val				
	415		420	425
AAC GAT TTT GAA GTC ATA CCC TTC GGT GCC GGG CGA				1347
Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg				
	435		440	
GGG ATG AGC TTG GGC CTG CGT ATG GTC CAT TTA ATG				1395
Gly Met Ser Leu Gly Leu Arg Met Val His Leu Met				
	450		455	
GTC CAC GCA TTT AAT TGG GCC TTG GCT GAT GGG CTG				1443
Val His Ala Phe Asn Trp Ala Leu Ala Asp Gly Leu				
	465		470	
TTA AAC ATG GAT GAA GCA TAT GGG CTC ACT CTA CAA				1491
Leu Asn Met Asp Glu Ala Tyr Gly Leu Thr Leu Gln				
	480		485	490

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CGA GCT GCA CCG TTA ATG GTG CAC CCG CGC ACC AGG CTG GCC CCA CAG	1539	
Arg Ala Ala Pro Leu Met Val His Pro Arg Thr Arg Leu Ala Pro Gln		
495	500	505
GCA TAT AAA ACT TCA TCA TCT TAATTAGAGA GCTATGTTCT GGGTGTGCC	1590	
Ala Tyr Lys Thr Ser Ser Ser		
510		
GGTTTGATGT CTCCATGTT TCTATTTAGG TTTAAATCTG TAAGATAAGG TGATTCTATG	1650	
CTGAATCACA AAAGTTGCTA TCTAAATTCC ATGTCCAATG AAAACGTTCT TCTTCCCTTC	1710	
TTATAATTAA TGAATACTTA TGATATAGGC GACAGCAA	1748	

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Phe Leu Ile Val Val Ile Thr Phe Leu Phe Ala Val Phe Leu Phe			
1	5	10	15

Arg Leu Leu Phe Ser Gly Lys Ser Gln Arg His Ser Leu Pro Leu Pro		
20	25	30

Pro Gly Pro Lys Pro Trp Pro Val Val Gly Asn Leu Pro His Leu Gly		
35	40	45

Pro Phe Pro His His Ser Ile Ala Glu Leu Ala Lys Lys His Gly Pro		
50	55	60

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Leu Met His Leu Arg Leu Gly Tyr Val Asp Val Val Val Ala Ala Ser
65 70 75 80

Ala Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn Phe Ser
85 90 95

Ser Arg Pro Pro Asn Ser Gly Ala Lys His Leu Ala Tyr Asn Tyr Gln
100 105 110

Asp Leu Val Phe Arg Pro Tyr Gly Pro Arg Trp Arg Met Phe Arg Lys
115 120 125

Ile Ser Ser Val His Leu Phe Ser Gly Lys Ala Leu Asp Asp Leu Lys
130 135 140

His Val Arg Gln Glu Glu Val Ser Val Leu Ala His Ala Leu Ala Asn
145 150 155 160

Ser Gly Ser Lys Val Val Asn Leu Ala Gln Leu Leu Asn Leu Cys Thr
165 170 175

Val Asn Ala Leu Gly Arg Val Met Val Gly Arg Arg Val Phe Gly Asp
180 185 190

Gly Ser Gly Gly Asp Asp Pro Lys Ala Asp Glu Phe Lys Ser Met Val
195 200 205

Val Glu Met Met Val Leu Ala Gly Val Phe Asn Ile Gly Asp Phe Ile
210 215 220

Pro Ser Leu Glu Trp Leu Asp Leu Gln Gly Val Ala Ser Lys Met Lys
225 230 235 240

Lys Leu His Lys Arg Phe Asp Asp Phe Leu Thr Ala Ile Val Glu Asp
245 250 255

His Lys Lys Gly Ser Gly Thr Ala Gly His Val Asp Met Leu Thr Thr

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260

265

270

Leu Leu Ser Leu Lys Glu Asp Ala Asp Gly Glu Gly Lys Leu Thr
275 280 285

Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Met Phe Thr Ala Gly Thr
290 295 300

Asp Thr Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg
305 310 315 320

His Pro His Met Leu Ala Arg Val Gln Lys Glu Leu Asp Asp Phe Val
325 330 335

Gly His Asp Arg Leu Val Thr Glu Ser Asp Ile Pro Asn Leu Pro Tyr
340 345 350

Leu Gln Ala Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro
355 360 365

Leu Ser Leu Pro Arg Met Ala Ala Glu Ser Cys Glu Ile Asn Gly Tyr
370 375 380

His Ile Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ser
385 390 395 400

Arg Asp Pro Ala Glu Trp Ala Asp Pro Leu Glu Phe Lys Pro Glu Arg
405 410 415

Phe Leu Pro Gly Gly Glu Lys Pro Asn Val Asp Ile Arg Gly Asn Asp
420 425 430

Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met
435 440 445

Ser Leu Gly Leu Arg Met Val His Leu Met Thr Ala Thr Leu Val His
450 455 460

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Ala Phe Asn Trp Ala Leu Ala Asp Gly Leu Thr Ala Glu Lys Leu Asn
 465 470 475 480

Met Asp Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ala Pro Leu Met
 485 490 495

Val His Pro Arg Thr Arg Leu Ala Pro Gln Ala Tyr Lys Thr Ser Ser
 500 505 510

Ser

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..1528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AAA ATG ACC ATT TTA GCT TTC GTA TTT TAC GCC CTC ATC CTC GGG TCA 48
 Met Thr Ile Leu Ala Phe Val Phe Tyr Ala Leu Ile Leu Gly Ser
 1 5 10 15

GTA CTC TAT GTA TTT CTT AAC TTA AGT TCA CGT AAA TCC GCC AGA CTC 96

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Val Leu Tyr Val Phe Leu Asn Leu Ser Ser Arg Lys Ser Ala Arg Leu			
20	25	30	
CCA CCC GGG CCA ACA CCA TGG CCT ATA GTC GGG AAC TTA CCA CAC CTT			144
Pro Pro Gly Pro Thr Pro Trp Pro Ile Val Gly Asn Leu Pro His Leu			
35	40	45	
GGC CCA ATC CCA CAC CAC GCA CTC GCG GCC TTA GCC AAG AAG TAC GGG			192
Gly Pro Ile Pro His His Ala Leu Ala Leu Ala Lys Lys Tyr Gly			
50	55	60	
CCA TTG ATG CAC CTG CGG CTC GGG TGT GTG GAC GTG GTT GTG GCC GCG			240
Pro Leu Met His Leu Arg Leu Gly Cys Val Asp Val Val Val Ala Ala			
65	70	75	
TCT GCT TCC GTA GCT GCA CAG TTT TTA AAA GTT CAC GAC GCA AAT TTT			288
Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Val His Asp Ala Asn Phe			
80	85	90	95
GCT AGT AGG CCG CCA AAT TCT GGC GCG AAA CAT GTG GCG TAT AAT TAT			336
Ala Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr Asn Tyr			
100	105	110	
CAG GAT CTT GTG TTT GCA CCT TAT GGT CCA AGG TGG CGT TTG TTA AGG			384
Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Leu Leu Arg			
115	120	125	
AAG ATT TGT TCG GTC CAT TTG TTT TCT GCT AAA GCA CTT GAT GAT TTT			432
Lys Ile Cys Ser Val His Leu Phe Ser Ala Lys Ala Leu Asp Asp Phe			
130	135	140	
CGT CAT GTT CGA CAG GAG GAG GTA GCA GTC CTA ACC CGC GTA CTA CTG			480
Arg His Val Arg Gln Glu Glu Val Ala Val Leu Thr Arg Val Leu Leu			
145	150	155	
AGT GCT GGA AAC TCA CCG GTA CAG CTT GGC CAA CTA CTT AAC GTG TGT			528
Ser Ala Gly Asn Ser Pro Val Gln Leu Gly Gln Leu Leu Asn Val Cys			

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160	165	170	175	
				576
GCC ACA AAC GCC TTA GCA CGG GTA ATG TTA GGT AGG AGA GTT TTC GGA Ala Thr Asn Ala Leu Ala Arg Val Met Leu Gly Arg Arg Val Phe Gly				
180	185	190		
				624
GAC GGA ATT GAC AGG TCA GCC AAT GAG TTC AAA GAT ATG GTA GTA GAG Asp Gly Ile Asp Arg Ser Ala Asn Glu Phe Lys Asp Met Val Val Glu				
195	200	205		
				672
TTA ATG GTA TTA GCA GGA GAA TTT AAC CTT GGT GAC TTT ATT CCT GTA Leu Met Val Leu Ala Gly Glu Phe Asn Leu Gly Asp Phe Ile Pro Val				
210	215	220		
				720
CTT GAC CTA TTC GAC CTA CAA GGC ATT ACT AAA AAA ATG AAG AAG CTT Leu Asp Leu Phe Asp Leu Gln Gly Ile Thr Lys Lys Met Lys Lys Leu				
225	230	235		
				768
CAT GTT CGG TTC GAT TCA TTT CTT AGT AAG ATC GTT GAG GAG CAT AAA His Val Arg Phe Asp Ser Phe Leu Ser Lys Ile Val Glu Glu His Lys				
240	245	250	255	
				816
ACG GCA CCT GGT GGG TTG GGT CAT ACT GAT TTG CTG AGC ACG TTG ATT Thr Ala Pro Gly Gly Leu Gly His Thr Asp Leu Leu Ser Thr Leu Ile				
260	265	270		
				864
TCA CTT AAA GAT GAT GCT GAT ATT GAA GGT GGG AAG CTT ACA GAT ACT Ser Leu Lys Asp Asp Ala Asp Ile Glu Gly Gly Lys Leu Thr Asp Thr				
275	280	285		
				912
GAA ATC AAA GCT TTG CTT CTG AAT TTA TTC GCT GCG GGA ACA GAC ACA Glu Ile Lys Ala Leu Leu Asn Leu Phe Ala Ala Gly Thr Asp Thr				
290	295	300		
				960
TCC TCT AGT ACA GTA GAA TGG GCA ATA GCC GAA CTC ATT CGT CAT CCA Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg His Pro				
305	310	315		

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CAA ATA TTA AAA CAA GCC CGA GAA GAG ATA GAC GCT GTA GTT GGT CAA Gln Ile Leu Lys Gln Ala Arg Glu Glu Ile Asp Ala Val Val Gly Gln	320	325	330	335	1008
GAC CGG CTT GTA ACA GAA TTG GAC TTG AGC CAA CTA ACA TAC CTC CAG Asp Arg Leu Val Thr Glu Leu Asp Leu Ser Gln Leu Thr Tyr Leu Gln		340	345	350	1056
GCT CTT GTG AAA GAG GTG TTT AGG CTC CAC CCT TCA ACG CCA CTC TCC Ala Leu Val Lys Glu Val Phe Arg Leu His Pro Ser Thr Pro Leu Ser		355	360	365	1104
TTA CCA AGA ATA TCA TCC GAG AGT TGT GAG GTC GAT GGG TAT TAT ATC Leu Pro Arg Ile Ser Ser Glu Ser Cys Glu Val Asp Gly Tyr Tyr Ile		370	375	380	1152
CCT AAG GGA TCC ACA CTC CTC GTT AAC GTG TGG GCC ATT GCG CGA GAC Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp		385	390	395	1200
CCA AAA ATG TGG GCG GAT CCT CTT GAA TTT AGG CCT TCT CGG TTT TTA Pro Lys Met Trp Ala Asp Pro Leu Glu Phe Arg Pro Ser Arg Phe Leu		400	405	410	415
CCC GGG GGA GAA AAG CCC GGT GCT GAT GTT AGG GGA AAT GAT TTT GAA Pro Gly Gly Glu Lys Pro Gly Ala Asp Val Arg Gly Asn Asp Phe Glu		420	425	430	1296
GTT ATA CCA TTT GGG GCA GGA CGA AGG ATT TGT GCG GGT ATG AGC CTA Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu		435	440	445	1344
GGC TTG AGA ATG GTC CAG TTG CTC ATT GCA ACA TTG GTC CAA ACT TTT Gly Leu Arg Met Val Gln Leu Leu Ile Ala Thr Leu Val Gln Thr Phe		450	455	460	1392
GAT TGG GAA CTG GCT AAC GGG TTA GAG CCG GAG ATG CTC AAC ATG GAA					1440

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Asp Trp Glu Leu Ala Asn Gly Leu Glu Pro Glu Met Leu Asn Met Glu			
465	470	475	
GAA GCG TAT GGA TTG ACC CTT CAA CGG GCT GCA CCC TTG ATG GTT CAC			
Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ala Pro Leu Met Val His			
480	485	490	495
CCG AAG CCG AGG TTA GCT CCC CAC GTA TAT GAA AGT ATT T AAGGACTAGT			
Pro Lys Pro Arg Leu Ala Pro His Val Tyr Glu Ser Ile			
500	505		
TTCTCTTTG CCTTTTGTT TCGCAAAGGT TAATGAATAA ACGATTTCAT GACTCAGATA			
GTTATGTAAA CAATTGTGTT TGCTGTTAT ATATTTATCT ATTTTTCTAG AACAAAAAAA			
AA			1660

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Thr Ile Leu Ala Phe Val Phe Tyr Ala Leu Ile Leu Gly Ser Val			
1	5	10	15

Leu Tyr Val Phe Leu Asn Leu Ser Ser Arg Lys Ser Ala Arg Leu Pro			
20	25	30	

Pro Gly Pro Thr Pro Trp Pro Ile Val Gly Asn Leu Pro His Leu Gly			
35	40	45	

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Pro Ile Pro His His Ala Leu Ala Ala Leu Ala Lys Lys Tyr Gly Pro
50 55 60

Leu Met His Leu Arg Leu Gly Cys Val Asp Val Val Val Ala Ala Ser
65 70 75 80

Ala Ser Val Ala Ala Gln Phe Leu Lys Val His Asp Ala Asn Phe Ala
85 90 95

Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr Asn Tyr Gln
100 105 110

Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Leu Leu Arg Lys
115 120 125

Ile Cys Ser Val His Leu Phe Ser Ala Lys Ala Leu Asp Asp Phe Arg
130 135 140

His Val Arg Gln Glu Glu Val Ala Val Leu Thr Arg Val Leu Leu Ser
145 150 155 160

Ala Gly Asn Ser Pro Val Gln Leu Gly Gln Leu Leu Asn Val Cys Ala
165 170 175

Thr Asn Ala Leu Ala Arg Val Met Leu Gly Arg Arg Val Phe Gly Asp
180 185 190

Gly Ile Asp Arg Ser Ala Asn Glu Phe Lys Asp Met Val Val Glu Leu
195 200 205

Met Val Leu Ala Gly Glu Phe Asn Leu Gly Asp Phe Ile Pro Val Leu
210 215 220

Asp Leu Phe Asp Leu Gln Gly Ile Thr Lys Lys Met Lys Lys Leu His
225 230 235 240

Val Arg Phe Asp Ser Phe Leu Ser Lys Ile Val Glu Glu His Lys Thr

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245

250

255

Ala Pro Gly Gly Leu Gly His Thr Asp Leu Leu Ser Thr Leu Ile Ser

260

265

270

Leu Lys Asp Asp Ala Asp Ile Glu Gly Gly Lys Leu Thr Asp Thr Glu

275

280

285

Ile Lys Ala Leu Leu Leu Asn Leu Phe Ala Ala Gly Thr Asp Thr Ser

290

295

300

Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg His Pro Gln

305

310

315

320

Ile Leu Lys Gln Ala Arg Glu Glu Ile Asp Ala Val Val Gly Gln Asp

325

330

335

Arg Leu Val Thr Glu Leu Asp Leu Ser Gln Leu Thr Tyr Leu Gln Ala

340

345

350

Leu Val Lys Glu Val Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu

355

360

365

Pro Arg Ile Ser Ser Glu Ser Cys Glu Val Asp Gly Tyr Tyr Ile Pro

370

375

380

Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp Pro

385

390

395

400

Lys Met Trp Ala Asp Pro Leu Glu Phe Arg Pro Ser Arg Phe Leu Pro

405

410

415

Gly Gly Glu Lys Pro Gly Ala Asp Val Arg Gly Asn Asp Phe Glu Val

420

425

430

Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu Gly

435

440

445

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Leu Arg Met Val Gln Leu Leu Ile Ala Thr Leu Val Gln Thr Phe Asp
450 455 460

Trp Glu Leu Ala Asn Gly Leu Glu Pro Glu Met Leu Asn Met Glu Glu
465 470 475 480

Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ala Pro Leu Met Val His Pro
485 490 495

Lys Pro Arg Leu Ala Pro His Val Tyr Glu Ser Ile
500 505

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 107..1631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTAAATTAAT TAATAAATAC ACACACCGACG AGATGTATGT AATGTAATGT AATATTATTA 60

CATACATCAT CACCGAATAC GCACGCTACT ACCACTGCGA TTAGCC ATG AGT CCC 115
Met Ser Pro

1

TTA GCC TTG ATG ATC ATA AGT ACC TTA TTA GGG TTT CTC CTA TAC CAC 163

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Leu Ala Leu Met Ile Ile Ser Thr Leu Leu Gly Phe Leu Leu Tyr His

5 10 15

TCT CTT CGC TTA CTA CTC TTC TCC GGC CAA GGT CGC CGA CTA CTA CCA 211
Ser Leu Arg Leu Leu Leu Phe Ser Gly Gln Gly Arg Arg Leu Leu Pro
20 25 30 35

CCA GGT CCA CGC CCG TGG CCG CTG GTG GGA AAT CTC CCG CAC TTA GGC 259
Pro Gly Pro Arg Pro Trp Pro Leu Val Gly Asn Leu Pro His Leu Gly
40 45 50

CCG AAG CCA CAC GCC TCC ATG GCC GAG CTC GCG CGA GCC TAC GGA CCC 307
Pro Lys Pro His Ala Ser Met Ala Glu Leu Ala Arg Ala Tyr Gly Pro
55 60 65

CTC ATG CAC CTA AAG ATG GGG TTC GTC CAC GTC GTG GTG GCT TCG TCG 355
Leu Met His Leu Lys Met Gly Phe Val His Val Val Val Ala Ser Ser
70 75 80

GCG AGC GCG GCG GAG CAG TGC CTG AGG GTT CAC GAC GCG AAT TTC TTG 403
Ala Ser Ala Ala Glu Gln Cys Leu Arg Val His Asp Ala Asn Phe Leu
85 90 95

AGC AGG CCA CCC AAC TCC GGC GCC AAG CAC GTC GCT TAC AAC TAC GAG 451
Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr Asn Tyr Glu
100 105 110 115

GAC TTG GTT TTC AGA CCG TAC GGT CCC AAG TGG AGG CTG TTG AGG AAG 499
Asp Leu Val Phe Arg Pro Tyr Gly Pro Lys Trp Arg Leu Leu Arg Lys
120 125 130

ATA TGC GCT CAG CAT ATT TTC TCC GTC AAG GCT ATG GAT GAC TTC AGG 547
Ile Cys Ala Gln His Ile Phe Ser Val Lys Ala Met Asp Asp Phe Arg
135 140 145

CGC GTC AGA GAG GAA GAG GTG GCC ATC CTG AGT CGC GCT CTA GCA GGC 595
Arg Val Arg Glu Glu Glu Val Ala Ile Leu Ser Arg Ala Leu Ala Gly

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150	155	160	
AAA AGG GCC GTA CCC ATA GGC CAA ATG CTC AAC GTG TGC GCC ACA AAC Lys Arg Ala Val Pro Ile Gly Gln Met Leu Asn Val Cys Ala Thr Asn			643
165	170	175	
GCC CTA TCT CGC GTC ATG ATG GGG CGG CGC GTG GTG GGC CAC GCG GAT Ala Leu Ser Arg Val Met Met Gly Arg Arg Val Val Gly His Ala Asp			691
180	185	190	195
GGA ACC AAC GAC GCC AAG GCG GAG GAG TTC AAA GCC ATG GTC GTC GAG Gly Thr Asn Asp Ala Lys Ala Glu Glu Phe Lys Ala Met Val Val Glu			739
200	205	210	
CTC ATG GTC CTC TCC GGC GTC TTC AAC ATC GGT GAT TTC ATC CCC TTC Leu Met Val Leu Ser Gly Val Phe Asn Ile Gly Asp Phe Ile Pro Phe			787
215	220	225	
CTC GAG CCT CTC GAC TTG CAG GGA GTG GCT TCC AAG ATG AAG AAA CTC Leu Glu Pro Leu Asp Leu Gln Gly Val Ala Ser Lys Met Lys Lys Leu			835
230	235	240	
CAC GCG CGG TTC GAT GCA TTC TTG ACC GAG ATT GTA CGA GAG CGT TGT His Ala Arg Phe Asp Ala Phe Leu Thr Glu Ile Val Arg Glu Arg Cys			883
245	250	255	
CAT GGG CAG ATC AAC AAC AGT GGT GCT CAT CAG GAT GAT TTG CTT AGC His Gly Gln Ile Asn Asn Ser Gly Ala His Gln Asp Asp Leu Leu Ser			931
260	265	270	275
ACG TTG ATT TCG TTC AAA GGG CTT GAC GAT GGC GAT GGT TCC AGG CTC Thr Leu Ile Ser Phe Lys Gly Leu Asp Asp Gly Asp Gly Ser Arg Leu			979
280	285	290	
ACT GAC ACA GAA ATC AAG GCG CTG CTC TTG AAC CTT TTG GAC ACG ACG Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Leu Asp Thr Thr			1027
295	300	305	

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TCG AGC ACG GTG GAA TGG GCC GTA GCC GAA CTC CTA CGC CAC CCT AAG			1075
Ser Ser Thr Val Glu Trp Ala Val Ala Glu Leu Leu Arg His Pro Lys			
310	315	320	
ACA TTA GCC CAA GTC CGG CAA GAG CTC GAC TCG GTC GTG GGT AAG AAC			1123
Thr Leu Ala Gln Val Arg Gln Glu Leu Asp Ser Val Val Gly Lys Asn			
325	330	335	
AGG CTC GTG TCC GAG ACC GAT CTG AAT CAG CTG CCC TAT CTA CAA GCT			1171
Arg Leu Val Ser Glu Thr Asp Leu Asn Gln Leu Pro Tyr Leu Gln Ala			
340	345	350	355
GTC GTC AAA GAA ACT TTC CGC CTC CAT CCT CCG ACG CCG CTC TCT CTA			1219
Val Val Lys Glu Thr Phe Arg Leu His Pro Pro Thr Pro Leu Ser Leu			
360	365	370	
CCG AGA CTC GCG GAA GAT GAT TGC GAG ATC GAC GGA TAC CTC ATC CCC			1267
Pro Arg Leu Ala Glu Asp Asp Cys Glu Ile Asp Gly Tyr Leu Ile Pro			
375	380	385	
AAG GGC TCG ACC CTT CTG GTG AAC GTT TGG GCC ATA GCC CGC GAT CCC			1315
Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp Pro			
390	395	400	
AAG GTT TGG GCC GAT CCG TTG GAG TTT AGG CCC GAA CGA TTC TTG ACG			1363
Lys Val Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe Leu Thr			
405	410	415	
GGC GGA GAA AAG GCC GAC GTC GAT GTC AAG GGG AAC GAT TTC GAA GTG			1411
Gly Gly Glu Lys Ala Asp Val Asp Val Lys Gly Asn Asp Phe Glu Val			
420	425	430	435
ATA CCG TTC GGG GCG GGT CGT AGG ATC TGC GCT GGC GTT GGC TTG GGA			1459
Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Val Gly Leu Gly			
440	445	450	
ATA CGT ATG GTC CAA CTG TTG ACG GCG AGT TTG ATC CAT GCA TTC GAT			1507

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Ile Arg Met Val Gln Leu Leu Thr Ala Ser Leu Ile His Ala Phe Asp			
455	460	465	
CTG GAC CTT GCT AAT GGG CTT TTG GCC CAA AAT CTG AAC ATG GAA GAA			1555
Leu Asp Leu Ala Asn Gly Leu Leu Ala Gln Asn Leu Asn Met Glu Glu			
470	475	480	
GCA TAT GGG CTT ACG CTA CAA CGG GCT GAG CCT TTG TTG GTC CAC CCT			1603
Ala Tyr Gly Leu Thr Leu Gln Arg Ala Glu Pro Leu Leu Val His Pro			
485	490	495	
AGG CCG CGG TTG GCC ACT CAT GTC TAT T AATTAAATTA GGCTTAAACT			1651
Arg Pro Arg Leu Ala Thr His Val Tyr			
500	505		
ACGATGAATG ACCCATTAA CGTTAATAAG AGTTTCAAT TTATGTGAGT TTGCATGGTA			1711
TGGTATGGTA TGGTGCTTGT AATAAATTGT ATCTGTTAGG TGTGTTCATT GATGATAAAT			1771
CTAGTTGTA CTGCTGCTCA AAAAAAAA AAAAAAAA AAAA			1815

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ser Pro Leu Ala Leu Met Ile Ile Ser Thr Leu Leu Gly Phe Leu			
1	5	10	15

Leu Tyr His Ser Leu Arg Leu Leu Leu Phe Ser Gly Gln Gly Arg Arg

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20

25

30

Leu Leu Pro Pro Gly Pro Arg Pro Trp Pro Leu Val Gly Asn Leu Pro

35

40

45

His Leu Gly Pro Lys Pro His Ala Ser Met Ala Glu Leu Ala Arg Ala

50

55

60

Tyr Gly Pro Leu Met His Leu Lys Met Gly Phe Val His Val Val Val

65

70

75

80

Ala Ser Ser Ala Ser Ala Ala Glu Gln Cys Leu Arg Val His Asp Ala

85

90

95

Asn Phe Leu Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr

100

105

110

Asn Tyr Glu Asp Leu Val Phe Arg Pro Tyr Gly Pro Lys Trp Arg Leu

115

120

125

Leu Arg Lys Ile Cys Ala Gln His Ile Phe Ser Val Lys Ala Met Asp

130

135

140

Asp Phe Arg Arg Val Arg Glu Glu Val Ala Ile Leu Ser Arg Ala

145

150

155

160

Leu Ala Gly Lys Arg Ala Val Pro Ile Gly Gln Met Leu Asn Val Cys

165

170

175

Ala Thr Asn Ala Leu Ser Arg Val Met Met Gly Arg Arg Val Val Gly

180

185

190

His Ala Asp Gly Thr Asn Asp Ala Lys Ala Glu Glu Phe Lys Ala Met

195

200

205

Val Val Glu Leu Met Val Leu Ser Gly Val Phe Asn Ile Gly Asp Phe

210

215

220

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Ile Pro Phe Leu Glu Pro Leu Asp Leu Gln Gly Val Ala Ser Lys Met
225 230 235 240

Lys Lys Leu His Ala Arg Phe Asp Ala Phe Leu Thr Glu Ile Val Arg
245 250 255

Glu Arg Cys His Gly Gln Ile Asn Asn Ser Gly Ala His Gln Asp Asp
260 265 270

Leu Leu Ser Thr Leu Ile Ser Phe Lys Gly Leu Asp Asp Gly Asp Gly
275 280 285

Ser Arg Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Asn Leu Leu
290 295 300

Asp Thr Thr Ser Ser Thr Val Glu Trp Ala Val Ala Glu Leu Leu Arg
305 310 315 320

His Pro Lys Thr Leu Ala Gln Val Arg Gln Glu Leu Asp Ser Val Val
325 330 335

Gly Lys Asn Arg Leu Val Ser Glu Thr Asp Leu Asn Gln Leu Pro Tyr
340 345 350

Leu Gln Ala Val Val Lys Glu Thr Phe Arg Leu His Pro Pro Thr Pro
355 360 365

Leu Ser Leu Pro Arg Leu Ala Glu Asp Asp Cys Glu Ile Asp Gly Tyr
370 375 380

Leu Ile Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala
385 390 395 400

Arg Asp Pro Lys Val Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg
405 410 415

Phe Leu Thr Gly Gly Glu Lys Ala Asp Val Asp Val Lys Gly Asn Asp

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420

425

430

Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Val

435

440

445

Gly Leu Gly Ile Arg Met Val Gln Leu Leu Thr Ala Ser Leu Ile His

450

455

460

Ala Phe Asp Leu Asp Leu Ala Asn Gly Leu Leu Ala Gln Asn Leu Asn

465

470

475

480

Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Glu Pro Leu Leu

485

490

495

Val His Pro Arg Pro Arg Leu Ala Thr His Val Tyr

500

505

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1824 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

G AGC TTA ACC TTA ATT TTC TGC ACT TTA GTT TTT GCA ATC TTT CTA
Ser Leu Thr Leu Ile Phe Cys Thr Leu Val Phe Ala Ile Phe Leu

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1	5	10	15		
TAT	TTT	CTT	ATT	CTC AGG GTG AAA CAG CGT TAC CCT CCT TTA CCT CTC CCA	94
Tyr	Phe	Leu	Ile	Leu Arg Val Lys Gln Arg Tyr Pro Leu Pro Leu Pro	
	20		25		30
CCC	GGA	CCA	AAA	CCA TGG CCG GTG TTA GGA AAC CTT CCC CAC CTG GGC	142
Pro	Gly	Pro	Lys	Pro Trp Pro Val Leu Gly Asn Leu Pro His Leu Gly	
	35		40		45
AAG	AAG	CCT	CAC	CAG TCG ATT GCG GCC ATG GCT GAG AGG TAC GGC CCC	190
Lys	Lys	Pro	His	Gln Ser Ile Ala Ala Met Ala Glu Arg Tyr Gly Pro	
	50		55		60
CTC	ATG	CAC	CTC	CGC CTA GGA TTC GTG GAC GTG GTT GTG GCC GCC TCC	238
Leu	Met	His	Leu	Arg Leu Gly Phe Val Asp Val Val Val Ala Ala Ser	
	65		70		75
GCC	GCC	GTG	GCC	GCT CAG TTC TTG AAA GTT CAC GAC TCG AAC TTC TCC	286
Ala	Ala	Val	Ala	Ala Gln Phe Leu Lys Val His Asp Ser Asn Phe Ser	
	80		85		90
AAC	CGG	CCG	CCG	AAC TCC GGC GCG GAA CAC ATT GCT TAT AAC TAT CAA	334
Asn	Arg	Pro	Pro	Asn Ser Gly Ala Glu His Ile Ala Tyr Asn Tyr Gln	
	100		105		110
GAC	CTC	GTC	TTC	GCG CCC TAC GGC CCG CGG TGG CGC ATG CTT AGG AAG	382
Asp	Leu	Val	Phe	Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu Arg Lys	
	115		120		125
ATC	ACC	TCC	GTG	CAT CTC TTC TCG GCC AAG GCG TTG GAT GAC TTC TGC	430
Ile	Thr	Ser	Val	His Leu Phe Ser Ala Lys Ala Leu Asp Asp Phe Cys	
	130		135		140
CAT	GTT	CGC	CAG	GAA GAG GTT GCA ACT CTG ACA CGC AGT CTA GCA AGT	478
His	Val	Arg	Gln	Glu Glu Val Ala Thr Leu Thr Arg Ser Leu Ala Ser	
	145		150		155

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GCA GGC AAA ACT CCA GTA AAA CTA GGG CAG TTA CTA AAC GTG TGC ACC			526
Ala Gly Lys Thr Pro Val Lys Leu Gly Gln Leu Leu Asn Val Cys Thr			
160	165	170	175
ACG AAC GCC CTA GCT CGT GTA ATG CTA GGG CGG AAG GTC TTT AAT GAC			574
Thr Asn Ala Leu Ala Arg Val Met Leu Gly Arg Lys Val Phe Asn Asp			
180	185	190	
GGA GGT AGC AAG AGC GAC CCA AAG GCG GAG GAG TTC AAG TCG ATG GTG			622
Gly Gly Ser Lys Ser Asp Pro Lys Ala Glu Glu Phe Lys Ser Met Val			
195	200	205	
GAG GAG ATG ATG GTG TTG GCC GGA AGT TTT AAC ATC GGC GAT TTC ATT			670
Glu Glu Met Met Val Leu Ala Gly Ser Phe Asn Ile Gly Asp Phe Ile			
210	215	220	
CCG GTC TTG GGT TGG TTT GAC GTT CAG GGT ATC GTA GGG AAG ATG AAG			718
Pro Val Leu Gly Trp Phe Asp Val Gln Gly Ile Val Gly Lys Met Lys			
225	230	235	
AAA CTA CAC GCG CGT TTT GAT GCG TTC TTG AAC ACC ATT CTA GAG GAA			766
Lys Leu His Ala Arg Phe Asp Ala Phe Leu Asn Thr Ile Leu Glu Glu			
240	245	250	255
CAC AAA TGT GTC AAC AAT CAA CAC ACG ACG TTG TCG AAA GAT GTG GAC			814
His Lys Cys Val Asn Asn Gln His Thr Thr Leu Ser Lys Asp Val Asp			
260	265	270	
TTC TTG AGC ACC CTA ATT AGG CTC AAA GAT AAT GGG GCT GAT ATG GAT			862
Phe Leu Ser Thr Leu Ile Arg Leu Lys Asp Asn Gly Ala Asp Met Asp			
275	280	285	
TGT GAA GAG GGA AAA CTC ACC GAC ACT GAA ATT AAG GCT TTG CTC TTG			910
Cys Glu Glu Gly Lys Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu			
290	295	300	
AAC CTG TTC ACA GCT GGG ACT GAT ACA TCA TCT AGC ACT GTG GAG TGG			958

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Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser Ser Ser Thr Val Glu Trp			
305	310	315	
GCA ATC GCA GAA CTA CTA CGC AAC CCA AAA ATC TTA AAC CAA GCA CAA			1006
Ala Ile Ala Glu Leu Leu Arg Asn Pro Lys Ile Leu Asn Gln Ala Gln			
320	325	330	335
CAA GAG CTT GAC TTA GTG GTG GGT CAA AAT CAG CTA GTC ACA GAA TCT			1054
Gln Glu Leu Asp Leu Val Val Gly Gln Asn Gln Leu Val Thr Glu Ser			
340	345	350	
GAC TTA ACC GAT CTA CCT TTC CTG CAA GCA ATA GTG AAG GAG ACC TTC			1102
Asp Leu Thr Asp Leu Pro Phe Leu Gln Ala Ile Val Lys Glu Thr Phe			
355	360	365	
AGG CTA CAC CCA ACC CCA CTC TCT CTT CCA AGA ATG GGA GCT CAG			1150
Arg Leu His Pro Ser Thr Pro Leu Ser Leu Pro Arg Met Gly Ala Gln			
370	375	380	
GGT TGC GAG ATC AAT GGC TAC TTC ATC CCC AAA GGC GCA ACG CTT TTG			1198
Gly Cys Glu Ile Asn Gly Tyr Phe Ile Pro Lys Gly Ala Thr Leu Leu			
385	390	395	
GTC AAC GTT TGG GCC ATA GCT CGT GAT CCC AAT GTG TGG ACA AAT CCT			1246
Val Asn Val Trp Ala Ile Ala Arg Asp Pro Asn Val Trp Thr Asn Pro			
400	405	410	415
CTT GAG TTC AAC CCA CAC CGA TTC TTG CCT GGT GGA GAA AAG CCC AAC			1294
Leu Glu Phe Asn Pro His Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn			
420	425	430	
GTG GAT ATT AAA GGG AAT GAC TTT GAA GTG ATT CCT TTT GGA GCC GGG			1342
Val Asp Ile Lys Gly Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly			
435	440	445	
CGT AGA ATA TGC TCT GGG ATG AGT TTG GGG ATA AGG ATG GTT CAC CTG			1390
Arg Arg Ile Cys Ser Gly Met Ser Leu Gly Ile Arg Met Val His Leu			

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450	455	460	
TTG GTT GCA ACT TTG GTG CAT GCT TTT GAT TGG GAT TTG GTG AAT GGA			1438
Leu Val Ala Thr Leu Val His Ala Phe Asp Trp Asp Leu Val Asn Gly			
465	470	475	
CAA TCT GTA GAG ACG CTC AAT ATG GAG GAA GCT TAT GGT CTC ACC CTT			1486
Gln Ser Val Glu Thr Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu			
480	485	490	495
CAA CGA GCT GTT CCT TTG ATG TTG CAT CCA AAG CCC AGA TTA CAA CCA			1534
Gln Arg Ala Val Pro Leu Met Leu His Pro Lys Pro Arg Leu Gln Pro			
500	505	510	
CAT CTC TAT ACT CTC AAT T AAATTGCAAT TTGATTGG TGATTATAACA			1583
His Leu Tyr Thr Leu Asn			
515			
ATTATAATCG AGGGACATAG GATCCCCATT TATTTATATT CAGTTATAAG AGACTTCCAA			1643
CAAAGGTCTA GCTTCGACC TTAAAAGTTG TAAAAGAGGT CCTACATATG TAAAAGCCCG			1703
CCAAAGGAAA ACTGGTTGTA TTCAATTCCG CTAGGCCTTG TCCGAAAGAC CTCATGAAGA			1763
CTACAAAGGT CATATATAAT GGTAAACCCA GTGTATTTGT TGTAAAAAAA AAAAAAAAAA			1823
A			1824

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ser Leu Thr Leu Ile Phe Cys Thr Leu Val Phe Ala Ile Phe Leu Tyr

1

5

10

15

Phe Leu Ile Leu Arg Val Lys Gln Arg Tyr Pro Leu Pro Leu Pro Pro

20

25

30

Gly Pro Lys Pro Trp Pro Val Leu Gly Asn Leu Pro His Leu Gly Lys

35

40

45

Lys Pro His Gln Ser Ile Ala Ala Met Ala Glu Arg Tyr Gly Pro Leu

50

55

60

Met His Leu Arg Leu Gly Phe Val Asp Val Val Val Ala Ala Ser Ala

65

70

75

80

Ala Val Ala Ala Gln Phe Leu Lys Val His Asp Ser Asn Phe Ser Asn

85

90

95

Arg Pro Pro Asn Ser Gly Ala Glu His Ile Ala Tyr Asn Tyr Gln Asp

100

105

110

Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu Arg Lys Ile

115

120

125

Thr Ser Val His Leu Phe Ser Ala Lys Ala Leu Asp Asp Phe Cys His

130

135

140

Val Arg Gln Glu Glu Val Ala Thr Leu Thr Arg Ser Leu Ala Ser Ala

145

150

155

160

Gly Lys Thr Pro Val Lys Leu Gly Gln Leu Leu Asn Val Cys Thr Thr

165

170

175

Asn Ala Leu Ala Arg Val Met Leu Gly Arg Lys Val Phe Asn Asp Gly

180

185

190

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Gly Ser Lys Ser Asp Pro Lys Ala Glu Glu Phe Lys Ser Met Val Glu
195 200 205

Glu Met Met Val Leu Ala Gly Ser Phe Asn Ile Gly Asp Phe Ile Pro
210 215 220

Val Leu Gly Trp Phe Asp Val Gln Gly Ile Val Gly Lys Met Lys Lys
225 230 235 240

Leu His Ala Arg Phe Asp Ala Phe Leu Asn Thr Ile Leu Glu Glu His
245 250 255

Lys Cys Val Asn Asn Gln His Thr Thr Leu Ser Lys Asp Val Asp Phe
260 265 270

Leu Ser Thr Leu Ile Arg Leu Lys Asp Asn Gly Ala Asp Met Asp Cys
275 280 285

Glu Glu Gly Lys Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn
290 295 300

Leu Phe Thr Ala Gly Thr Asp Thr Ser Ser Ser Thr Val Glu Trp Ala
305 310 315 320

Ile Ala Glu Leu Leu Arg Asn Pro Lys Ile Leu Asn Gln Ala Gln Gln
325 330 335

Glu Leu Asp Leu Val Val Gly Gln Asn Gln Leu Val Thr Glu Ser Asp
340 345 350

Leu Thr Asp Leu Pro Phe Leu Gln Ala Ile Val Lys Glu Thr Phe Arg
355 360 365

Leu His Pro Ser Thr Pro Leu Ser Leu Pro Arg Met Gly Ala Gln Gly
370 375 380

Cys Glu Ile Asn Gly Tyr Phe Ile Pro Lys Gly Ala Thr Leu Leu Val

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385

390

395

400

Asn Val Trp Ala Ile Ala Arg Asp Pro Asn Val Trp Thr Asn Pro Leu
405 410 415

Glu Phe Asn Pro His Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn Val
420 425 430

Asp Ile Lys Gly Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg
435 440 445

Arg Ile Cys Ser Gly Met Ser Leu Gly Ile Arg Met Val His Leu Leu
450 455 460

Val Ala Thr Leu Val His Ala Phe Asp Trp Asp Leu Val Asn Gly Gln
465 470 475 480

Ser Val Glu Thr Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln
485 490 495

Arg Ala Val Pro Leu Met Leu His Pro Lys Pro Arg Leu Gln Pro His
500 505 510

Leu Tyr Thr Leu Asn
515

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCC ATC CTC GGA AAC ATC CCC CAT CTC GGC TCC AAA CCG CAC CAA ACA	48	
Pro Ile Leu Gly Asn Ile Pro His Leu Gly Ser Lys Pro His Gln Thr		
1 5 10 15		
CTC GCG GAA ATG GCG AAA ACC TAC GGT CCG CTC ATG CAC TTG AAG TTC	96	
Leu Ala Glu Met Ala Lys Thr Tyr Gly Pro Leu Met His Leu Lys Phe		
20 25 30		
GGG CTT AAG GAC GCG GTG GTG GCG TCG TCT GCG TCG GTG GCA GAG CAG	144	
Gly Leu Lys Asp Ala Val Val Ala Ser Ser Ala Ser Val Ala Glu Gln		
35 40 45		
TTT CTG AAG AAA CAC GAC GTG AAT TTC TCG AAC CGG CCG CCA AAC TCC	192	
Phe Leu Lys Lys His Asp Val Asn Phe Ser Asn Arg Pro Pro Asn Ser		
50 55 60		
GGG GCC AAA CAT ATA GCT TAT AAC TAT CAG GAC CTG GTA TTC GCT CCC	240	
Gly Ala Lys His Ile Ala Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro		
65 70 75 80		
TAT GGA CCC CGG TGG CGG TTG CTT AGG AAA ATC TGT TCC GTC CAT CTT	288	
Tyr Gly Pro Arg Trp Arg Leu Leu Arg Lys Ile Cys Ser Val His Leu		
85 90 95		
TTC TCG TCT AAG GCC TTG GAT GAC TTT CAG CAT GTT CGA CAT GAG GAG	336	
Phe Ser Ser Lys Ala Leu Asp Asp Phe Gln His Val Arg His Glu Glu		
100 105 110		
ATA TGC ATC CTT ATA CGA GCA ATA GCG AGT GGC GGT CAT GCT CCG GTG	384	
Ile Cys Ile Leu Ile Arg Ala Ile Ala Ser Gly Gly His Ala Pro Val		

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115	120	125	
AAT TTA GGC AAG TTA TTA GGA GTG TGC ACA ACC AAT GCC CTG GCA AGA Asn Leu Gly Lys Leu Leu Gly Val Cys Thr Thr Asn Ala Leu Ala Arg			432
130	135	140	
GTG ATG CTT GGA AGA AGA GTA TTC GAA GGC GAC GGC GGC GAG AAT CCG Val Met Leu Gly Arg Arg Val Phe Glu Gly Asp Gly Gly Glu Asn Pro			480
145	150	155	160
CAT GCC GAC GAG TTT AAA TCA ATG GTG GTG GAG ATT ATG GTG TTA GCC His Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu Ala			528
165	170	175	
GGT GCA TTC AAC TTG GGT GAT TTC ATC CCG GTT CTA GAT TGG TTC GAT Gly Ala Phe Asn Leu Gly Asp Phe Ile Pro Val Leu Asp Trp Phe Asp			576
180	185	190	
TTG CAA GGA ATT GCT GGT AAA ATG AAG AAA CTT CAT GCC CGT TTC GAC Leu Gln Gly Ile Ala Gly Lys Met Lys Lys Leu His Ala Arg Phe Asp			624
195	200	205	
AAG TTT TTA AAT GGG ATC CTA GAA GAT CGT AAA TCT AAC GGC TCT AAT Lys Phe Leu Asn Gly Ile Leu Glu Asp Arg Lys Ser Asn Gly Ser Asn			672
210	215	220	
GGA GCT GAA CAA TAC GTG GAC TTG CTC AGT GTG TTG ATC TCT CTT CAA Gly Ala Glu Gln Tyr Val Asp Leu Leu Ser Val Leu Ile Ser Leu Gln			720
225	230	235	240
GAT AGT AAT ATC GAC GGT GGT GAC GAA GGA ACC AAA CTC ACA GAT ACT Asp Ser Asn Ile Asp Gly Gly Asp Glu Gly Thr Lys Leu Thr Asp Thr			768
245	250	255	
GAA ATC AAA GCT CTC CTT TTG AAC TTG TTC ATA GCC GGA ACA GAC ACT Glu Ile Lys Ala Leu Leu Asn Leu Phe Ile Ala Gly Thr Asp Thr			816
260	265	270	

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TCA TCA AGT ACT GTA GAA TGG GCC ATG GCA GAA CTA ATC CGA AAC CCA			864
Ser Ser Ser Thr Val Glu Trp Ala Met Ala Glu Leu Ile Arg Asn Pro			
275	280	285	
AAG TTA CTA GTC CAA GCC CAA GAA GAG CTA GAC AGA GTA GTC GGG CCG			912
Lys Leu Leu Val Gln Ala Gln Glu Glu Leu Asp Arg Val Val Gly Pro			
290	295	300	
AAC CGA TTC GTA ACC GAA TCT GAT CTT CCT CAA CTG ACA TTC CTT CAA			960
Asn Arg Phe Val Thr Glu Ser Asp Leu Pro Gln Leu Thr Phe Leu Gln			
305	310	315	320
GCC GTC ATC AAA GAG ACT TTC AGG CTT CAT CCA TCC ACC CCA CTC TCT			- 1008
Ala Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser			
325	330	335	
CTT CCA CGA ATG GCG GCG GAG GAC TGT GAG ATC AAT GGG TAT TAT GTC			1056
Leu Pro Arg Met Ala Ala Glu Asp Cys Glu Ile Asn Gly Tyr Tyr Val			
340	345	350	
TCA GAA GGT TCG ACA TTG CTC GTC AAT GTG TGG GCC ATA GCT CGT GAT			1104
Ser Glu Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp			
355	360	365	
CCA AAT GCG TGG GCC AAT CCA CTA GAT TTC AAC CCG ACT CGT TTC TTG			1152
Pro Asn Ala Trp Ala Asn Pro Leu Asp Phe Asn Pro Thr Arg Phe Leu			
370	375	380	
GCC GGT GGA GAG AAG CCT AAT GTT GAT GTT AAA GGG AAT GAT TTT GAA			1200
Ala Gly Gly Glu Lys Pro Asn Val Asp Val Lys Gly Asn Asp Phe Glu			
385	390	395	400
GTG ATA CCT TTC GGT GCT GGG CGC AGG ATA TGT GCC GGA ATG AGC TTA			1248
Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu			
405	410	415	
GGT ATA CGG ATG GTT CAA CTA GTA ACG GCT TCG TTA GTT CAT TCG TTT			1296

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Gly Ile Arg Met Val Gln Leu Val Thr Ala Ser Leu Val His Ser Phe
 420 425 430

GAT TGG GCT TTG TTG GAT GGA CTT AAA CCC GAG AAG CTT GAC ATG GAG 1344
 Asp Trp Ala Leu Leu Asp Gly Leu Lys Pro Glu Lys Leu Asp Met Glu
 435 440 445

GAA GGT TAT GGA CTA ACG CTT CAA CGA GCT TCA CCT TTA ATC GTC CAT 1392
 Glu Gly Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His
 450 455 460

CCA AAG CCG AGG CTC TCG GCT CAA GTT TAT TGT ATG T AACAAAGTTTG 1439
 Pro Lys Pro Arg Leu Ser Ala Gln Val Tyr Cys Met
 465 470 475

TGAAGCCAGT CTGATTCAG TTGGATTGT AGTTATTTA TGATCATTTG GTATTTATT 1499

TTGTATTCG GTTGAATACA ATAAAGGGAA GGTGGATCGT CTGCTGTATA ATAGCGACGT 1559

TTAACGTGT TGTGATAGTA CCGTGTNTA CTAAAACGAT GTCGTTGAT TTTTATAGT 1619

ATTAAAAAAA TAAACAGCTG GATTTGAAC CAAAAAAA AAAAAAAA 1667

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Pro Ile Leu Gly Asn Ile Pro His Leu Gly Ser Lys Pro His Gln Thr

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Leu Ala Glu Met Ala Lys Thr Tyr Gly Pro Leu Met His Leu Lys Phe
20 25 30

Gly Leu Lys Asp Ala Val Val Ala Ser Ser Ala Ser Val Ala Glu Gln
35 40 45

Phe Leu Lys His Asp Val Asn Phe Ser Asn Arg Pro Pro Asn Ser
50 55 60

Gly Ala Lys His Ile Ala Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro
65 70 75 80

Tyr Gly Pro Arg Trp Arg Leu Leu Arg Lys Ile Cys Ser Val His Leu
85 90 95

Phe Ser Ser Lys Ala Leu Asp Asp Phe Gln His Val Arg His Glu Glu
100 105 110

Ile Cys Ile Leu Ile Arg Ala Ile Ala Ser Gly Gly His Ala Pro Val
115 120 125

Asn Leu Gly Lys Leu Leu Gly Val Cys Thr Thr Asn Ala Leu Ala Arg
130 135 140

Val Met Leu Gly Arg Arg Val Phe Glu Gly Asp Gly Glu Asn Pro
145 150 155 160

His Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu Ala
165 170 175

Gly Ala Phe Asn Leu Gly Asp Phe Ile Pro Val Leu Asp Trp Phe Asp
180 185 190

Leu Gln Gly Ile Ala Gly Lys Met Lys Lys Leu His Ala Arg Phe Asp
195 200 205

Lys Phe Leu Asn Gly Ile Leu Glu Asp Arg Lys Ser Asn Gly Ser Asn

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210

215

220

Gly Ala Glu Gln Tyr Val Asp Leu Leu Ser Val Leu Ile Ser Leu Gln
225 230 235 240

Asp Ser Asn Ile Asp Gly Gly Asp Glu Gly Thr Lys Leu Thr Asp Thr
245 250 255

Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Ile Ala Gly Thr Asp Thr
260 265 270

Ser Ser Ser Thr Val Glu Trp Ala Met Ala Glu Leu Ile Arg Asn Pro
275 280 285

Lys Leu Leu Val Gln Ala Gln Glu Glu Leu Asp Arg Val Val Gly Pro
290 295 300

Asn Arg Phe Val Thr Glu Ser Asp Leu Pro Gln Leu Thr Phe Leu Gln
305 310 315 320

Ala Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser
325 330 335

Leu Pro Arg Met Ala Ala Glu Asp Cys Glu Ile Asn Gly Tyr Tyr Val
340 345 350

Ser Glu Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp
355 360 365

Pro Asn Ala Trp Ala Asn Pro Leu Asp Phe Asn Pro Thr Arg Phe Leu
370 375 380

Ala Gly Gly Glu Lys Pro Asn Val Asp Val Lys Gly Asn Asp Phe Glu
385 390 395 400

Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu
405 410 415

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Gly Ile Arg Met Val Gln Leu Val Thr Ala Ser Leu Val His Ser Phe
 420 425 430

Asp Trp Ala Leu Leu Asp Gly Leu Lys Pro Glu Lys Leu Asp Met Glu
 435 440 445

Glu Gly Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His
 450 455 460

Pro Lys Pro Arg Leu Ser Ala Gln Val Tyr Cys Met
 465 470 475

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1214 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

T CGC ATC CTC ACG CGA TCT ATA GCG AGT GCT GGG GAA AAT CCG ATT 46
 Arg Ile Leu Thr Arg Ser Ile Ala Ser Ala Gly Glu Asn Pro Ile
 1 5 10 15

AAC TTA GGT CAA TTA CTC GGG GTG TGT ACC ACA AAT GCT CTG GCG AGA 94
 Asn Leu Gly Gln Leu Leu Gly Val Cys Thr Thr Asn Ala Leu Ala Arg
 20 25 30

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GTG ATG CTT GGA AGG AGG GTA TTC GGC GAT GGG AGC GGC GGC GTA GAT			142
Val Met Leu Gly Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Val Asp			
35	40	45	
CCT CAG GCG GAC GAG TTC AAA TCC ATG GTG GTG GAA ATC ATG GTG TTG			190
Pro Gln Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu			
50	55	60	
GCC GGC GCG TTT AAT CTA GGT GAT TTT ATT CCC GCT CTT GAT TGG TTC			238
Ala Gly Ala Phe Asn Leu Gly Asp Phe Ile Pro Ala Leu Asp Trp Phe			
65	70	75	
GAT CTG CAG GGA ATT ACG GCA AAA ATG AAG AAA GTT CAC GCT CGT TTC			286
Asp Leu Gln Gly Ile Thr Ala Lys Met Lys Lys Val His Ala Arg Phe			
80	85	90	95
GAT GCG TTC TTA GAC GCG ATC CTT GAG GAG CAC AAA TCC AAC GGC TCT			334
Asp Ala Phe Leu Asp Ala Ile Leu Glu Glu His Lys Ser Asn Gly Ser			
100	105	110	
CGC GGA GCT AAG CAA CAC GTT GAC TTG CTG AGT ATG TTG ATC TCC CTT			382
Arg Gly Ala Lys Gln His Val Asp Leu Leu Ser Met Leu Ile Ser Leu			
115	120	125	
CAA GAT AAT AAC ATT GAT GGT GAA AGT GGC GCC AAA CTC ACT GAT ACA			430
Gln Asp Asn Asn Ile Asp Gly Glu Ser Gly Ala Lys Leu Thr Asp Thr			
130	135	140	
GAA ATC AAA GCT TTG CTT CTG AAC TTG TTC ACG GCT GGA ACA GAC ACG			478
Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr			
145	150	155	
TCA TCA AGT ACT GTG GAG TGG GCA ATC GCA GAG CTA ATC CGA AAC CCA			526
Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg Asn Pro			
160	165	170	175
GAA GTA TTG GTT CAA GCC CAA GAG CTC GAT AGA GTA GTT GGG CCA			574

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Glu Val Leu Val Gln Ala Gln Gln Glu Leu Asp Arg Val Val Gly Pro
180 185 190

AGT CGT CTT GTG ACC GAA TCT GAT CTG CCT CAA TTG GCA TTC CTT CAA 622
Ser Arg Leu Val Thr Glu Ser Asp Leu Pro Gln Leu Ala Phe Leu Gln
195 200 205

GCT GTC ATC AAA GAG ACT TTC AGA CTT CAT CCA TCC ACT CCA CTC TCT 670
Ala Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser
210 215 220

CTT CCA CGA ATG GCT TCA GAG GGT TGT GAA ATC AAT GGA TAC TCC ATC 718
Leu Pro Arg Met Ala Ser Glu Gly Cys Glu Ile Asn Gly Tyr Ser Ile
225 230 235

CCA AAG GGT TCG ACA TTG CTC GTT AAC GTA TGG TCC ATA GCC CGT GAT 766
Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ser Ile Ala Arg Asp
240 245 250 255

CCT AGT ATA TGG GCC GAC CCA TTA GAA TTT AGG CCG GCA CGT TTC TTG 814
Pro Ser Ile Trp Ala Asp Pro Leu Glu Phe Arg Pro Ala Arg Phe Leu
260 265 270

CCC GGC GGA GAA AAG CCC AAT GTT GAT GTG AGA GGC AAT GAT TTT GAG 862
Pro Gly Gly Glu Lys Pro Asn Val Asp Val Arg Gly Asn Asp Phe Glu
275 280 285

GTC ATA CCA TTT GGT GCT GGA CGT AGG ATA TGT GCT GGA ATG AGC TTG 910
Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu
290 295 300

GGT TTA AGA ATG GTT CAA CTT TCG ACA GCT ACT TTG GTT CAT TCG TTT 958
Gly Leu Arg Met Val Gln Leu Ser Thr Ala Thr Leu Val His Ser Phe
305 310 315

AAT TGG GAT TTG CTG AAT GGG ATG AGC CCA GAT AAA CTT GAC ATG GAA 1006
Asn Trp Asp Leu Leu Asn Gly Met Ser Pro Asp Lys Leu Asp Met Glu

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320

325

330

335

GAA GCT TAT GGG CTT ACA TTG CAA CGG GCT TCA CCT TTG ATT GTC CAC 1054
Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His

340

345

350

CCA AAG CCC AGG CTT GCT AGC TCT ATG TAT GTT AAA T GAAATTATGC 1101
Pro Lys Pro Arg Leu Ala Ser Ser Met Tyr Val Lys

355

360

TGTGCGAATA ATTCCATTATT TATAGCAGGA AATGTCATCT TGAATTATGT GTAATGTTCT 1161

TCTAACCTTC GATGGAAGTG CAAAACAAGT TTTATTAAAA AAAAAAAAAA AAA 1214

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Arg Ile Leu Thr Arg Ser Ile Ala Ser Ala Gly Glu Asn Pro Ile Asn
1 5 10 15

Leu Gly Gln Leu Leu Gly Val Cys Thr Thr Asn Ala Leu Ala Arg Val
20 25 30

Met Leu Gly Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Val Asp Pro
35 40 45

Gln Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu Ala
50 55 60

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Gly Ala Phe Asn Leu Gly Asp Phe Ile Pro Ala Leu Asp Trp Phe Asp
65 70 75 80

Leu Gln Gly Ile Thr Ala Lys Met Lys Lys Val His Ala Arg Phe Asp
85 90 95

Ala Phe Leu Asp Ala Ile Leu Glu Glu His Lys Ser Asn Gly Ser Arg
100 105 110

Gly Ala Lys Gln His Val Asp Leu Leu Ser Met Leu Ile Ser Leu Gln
115 120 125

Asp Asn Asn Ile Asp Gly Glu Ser Gly Ala Lys Leu Thr Asp Thr Glu
130 135 140

Ile Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser
145 150 155 160

Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg Asn Pro Glu
165 170 175

Val Leu Val Gln Ala Gln Gln Glu Leu Asp Arg Val Val Gly Pro Ser
180 185 190

Arg Leu Val Thr Glu Ser Asp Leu Pro Gln Leu Ala Phe Leu Gln Ala
195 200 205

Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu
210 215 220

Pro Arg Met Ala Ser Glu Gly Cys Glu Ile Asn Gly Tyr Ser Ile Pro
225 230 235 240

Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ser Ile Ala Arg Asp Pro
245 250 255

Ser Ile Trp Ala Asp Pro Leu Glu Phe Arg Pro Ala Arg Phe Leu Pro

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260

265

270

Gly Gly Glu Lys Pro Asn Val Asp Val Arg Gly Asn Asp Phe Glu Val
275 280 285

Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu Gly
290 295 300

Leu Arg Met Val Gln Leu Ser Thr Ala Thr Leu Val His Ser Phe Asn
305 310 315 320

Trp Asp Leu Leu Asn Gly Met Ser Pro Asp Lys Leu Asp Met Glu Glu
325 330 335

Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His Pro
340 345 350

Lys Pro Arg Leu Ala Ser Ser Met Tyr Val Lys
355 360

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1757 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 35..1522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

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CCGTTGCTGT CGAGAAAACA GAAAGAAGAG AAAA ATG GAC TAC GTG AAT ATT	52		
Met Asp Tyr Val Asn Ile			
1	5		
TTG CTG GGA CTG TTT TTC ACT TGG TTC TTG GTG AAT GGA CTC ATG TCA	100		
Leu Leu Gly Leu Phe Phe Thr Trp Phe Leu Val Asn Gly Leu Met Ser			
10	15	20	
CTT CGA AGA AGA AAA ATC TCT AAG AAA CTT CCA CCA GGT CCA TTT CCT	148		
Leu Arg Arg Arg Lys Ile Ser Lys Lys Leu Pro Pro Gly Pro Phe Pro			
25	30	35	
TTG CCT ATC ATC GGA AAT CTT CAC TTA CTT GGT AAT CAT CCT CAC AAA	196		
Leu Pro Ile Ile Gly Asn Leu His Leu Leu Gly Asn His Pro His Lys			
40	45	50	
TCA CTT GCT CAA CTT GCA AAA ATT CAT GGT CCT ATT ATG AAT CTC AAA	244		
Ser Leu Ala Gln Leu Ala Lys Ile His Gly Pro Ile Met Asn Leu Lys			
55	60	65	70
TTA GGC CAA CTA AAC ACA GTG GTC ATT TCA TCA TCA GTC GTG GCA AGA	292		
Leu Gly Gln Leu Asn Thr Val Val Ile Ser Ser Val Val Ala Arg			
75	80	85	
GAA GTC TTG CAA AAA CAA GAC TTA ACA TTT TCC AAT AGG TTT GTC CCG	340		
Glu Val Leu Gln Lys Gln Asp Leu Thr Phe Ser Asn Arg Phe Val Pro			
90	95	100	
GAC GTA GTC CAT GTC CGA AAT CAC TCC GAT TTT TCT GTT GTT TGG TTA	388		
Asp Val Val His Val Arg Asn His Ser Asp Phe Ser Val Val Trp Leu			
105	110	115	
CCA GTC AAT TCT CGA TGG AAA ACG CTT CGC AAA ATC ATG AAC TCT AGC	436		
Pro Val Asn Ser Arg Trp Lys Thr Leu Arg Lys Ile Met Asn Ser Ser			
120	125	130	
ATC TTT TCT GGT AAC AAG CTT GAT GGT AAT CAA CAT CTG AGG TCT AAA	484		

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Ile Phe Ser Gly Asn Lys Leu Asp Gly Asn Gln His Leu Arg Ser Lys				
135	140	145	150	
AAG GTC CAA GAG TTA ATT GAT TAT TGT CAA AAG TGT GCC AAG AAT GGC				532
Lys Val Gln Glu Leu Ile Asp Tyr Cys Gln Lys Cys Ala Lys Asn Gly				
155	160	165		
GAA GCA GTG GAT ATA GGA AGA GCA ACT TTT GGA ACT ACT TTG AAT TTG				580
Glu Ala Val Asp Ile Gly Arg Ala Thr Phe Gly Thr Thr Leu Asn Leu				
170	175	180		
CTA TCC AAC ACC ATT TTC TCT AAA GAT TTG ACT AAT CCG TTT TCT GAT				628
Leu Ser Asn Thr Ile Phe Ser Lys Asp Leu Thr Asn Pro Phe Ser Asp				
185	190	195		
TCT GCT AAA GAG TTT AAG GAA TTG GTT TGG AAC ATT ATG GTT GAG GCT				676
Ser Ala Lys Glu Phe Lys Glu Leu Val Trp Asn Ile Met Val Glu Ala				
200	205	210		
GGA AAA CCC AAT TTG GTG GAC TAC TTT CCT TTC CTT GAG AAA ATT GAT				724
Gly Lys Pro Asn Leu Val Asp Tyr Phe Pro Phe Leu Glu Lys Ile Asp				
215	220	225	230	
CCG CAA GGT ATA AAG CGA CGC ATG ACT AAT AAT TTT ACT AAG TTT CTT				772
Pro Gln Gly Ile Lys Arg Arg Met Thr Asn Asn Phe Thr Lys Phe Leu				
235	240	245		
GGC CTT ATC AGC GGT TTG ATT GAT GAC CGG TTA AAG GAA AGG AAT CTA				820
Gly Leu Ile Ser Gly Leu Ile Asp Asp Arg Leu Lys Glu Arg Asn Leu				
250	255	260		
AGG GAC AAT GCA AAT ATT GAT GTT TTA GAC GCC CTT CTC AAC ATT AGC				868
Arg Asp Asn Ala Asn Ile Asp Val Leu Asp Ala Leu Leu Asn Ile Ser				
265	270	275		
CAA GAG AAC CCA GAA GAG ATT GAC AGG AAT CAA ATC GAG CAG TTG TGT				916
Gln Glu Asn Pro Glu Glu Ile Asp Arg Asn Gln Ile Glu Gln Leu Cys				

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280	285	290	
CTG GAC TTG TTT GCA GCA GGG ACT GAT ACT ACA TCG AAT ACC TTG GAG			964
Leu Asp Leu Phe Ala Ala Gly Thr Asp Thr Thr Ser Asn Thr Leu Glu			
295	300	305	310
TGG GCA ATG GCA GAA CTA CTT CAG AAT CCA CAC ACA TTG CAG AAA GCA			1012
Trp Ala Met Ala Glu Leu Leu Gln Asn Pro His Thr Leu Gln Lys Ala			
315	320	325	
CAA GAA GAA CTT GCA CAA GTC ATT GGT AAA GGC AAA CAA GTA GAA GAA			1060
Gln Glu Glu Leu Ala Gln Val Ile Gly Lys Gly Lys Gln Val Glu Glu			
330	335	340	
GCA GAT GTT GGA CGA CTA CCT TAC TTG CGA TGC ATA GTG AAA GAA ACC			1108
Ala Asp Val Gly Arg Leu Pro Tyr Leu Arg Cys Ile Val Lys Glu Thr			
345	350	355	
TTA CGA ATA CAC CCA GCG GCT CCT CTC TTA ATT CCA CGT AAA GTG GAG			1156
Leu Arg Ile His Pro Ala Ala Pro Leu Leu Ile Pro Arg Lys Val Glu			
360	365	370	
GAA GAC GTT GAG TTG TCT ACC TAT ATT ATT CCA AAG GAT TCA CAA GTT			1204
Glu Asp Val Glu Leu Ser Thr Tyr Ile Ile Pro Lys Asp Ser Gln Val			
375	380	385	390
CTA GTG AAC GTA TGG GCA ATT GGA CGC AAC TCT GAT CTA TGG GAA AAT			1252
Leu Val Asn Val Trp Ala Ile Gly Arg Asn Ser Asp Leu Trp Glu Asn			
395	400	405	
CCT TTG GTC TTT AAG CCA GAA AGG TTT TGG GAG TCA GAA ATA GAT ATC			1300
Pro Leu Val Phe Lys Pro Glu Arg Phe Trp Glu Ser Glu Ile Asp Ile			
410	415	420	
CGA GGT CGA GAT TTT GAA CTC ATT CCA TTT GGT GCT GGT CGA AGA ATT			1348
Arg Gly Arg Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile			
425	430	435	

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TGC CCT GGA TTG CCT TTG GCT ATG AGG ATG ATT CCA GTA GCA CTA GGT	1396	
Cys Pro Gly Leu Pro Leu Ala Met Arg Met Ile Pro Val Ala Leu Gly		
440	445	450
TCA TTG CTA AAC TCA TTT AAT TGG AAA CTA TAT GGT GGA ATT GCA CCT	1444	
Ser Leu Leu Asn Ser Phe Asn Trp Lys Leu Tyr Gly Gly Ile Ala Pro		
455	460	465
AAA GAT TTG GAC ATG CAG GAA AAG TTT GGC ATT ACC TTG GCG AAA GCC	1492	
Lys Asp Leu Asp Met Gln Glu Lys Phe Gly Ile Thr Leu Ala Lys Ala		
475	480	485
CAA CCT CTG CTA GCT ATC CCA ACT CCC CTG TAGCTATAGG GATAAATTAA	1542	
Gln Pro Leu Leu Ala Ile Pro Thr Pro Leu		
490	495	
GTTGAGGTTT TAAGTTACTA GTAGATTCTA TTGCAGCTAT AGGATTTCTT TCACCATCAC	1602	
GTATGCTTTA CCGTTGGATG ATGGAAAGAA ATATCTATAG CTTTGGGTTT GTTAGTTG	1662	
CACATAAAAA TTGAATGAAT GGAATACCAT GGAGTTATAA GAAATAATAA GACTATGATT	1722	
CTTACCCCTAC TTGAACAATG ACATGGCTAT TTCAC	1757	

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

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TTTTTTTTTTT TTTTTTTA

18

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TTTTTTTTTTT TTTTTTTC

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTTTTTTTTT TTTTTTTG

18

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(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Trp Ala Ile Gly Arg Asp Pro

5

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGGGCIATIG GI(A/C)GIGA(T/C)CC

20

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(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Phe Arg Pro Glu Arg Phe

5

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 acids
- (B) TYPE: nucleic acids
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGGAATT(T/C) (A/C) G ICCIGA(A/G) (A/C) GI TT

22

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(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 nucleic acids
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCITT(T/C)GGIG CIGGI(A/C)GI(A/C)G IATITG(T/G)(C/G)CI GG

32

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu Phe Xaa Pro Glu Arg Phe

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(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 nucleic acids
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAITT(T/C)IIIIC CIGAI(A/C)GITT

20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 nucleic acids
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CCACACGAGT AGTTTGCGA TTTGACCC

28

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(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 nucleic acids
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GTCTTGGACA TCACACTTCA ATCTG

25

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 nucleic acids
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCGAATTCCC CCCCCCC

17

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 nucleic acids

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCIGG(A/G)CAIA TIC(G/T) (C/T) (C/T)TICC IGCICC(A/G)AAI GG

32